

# SEQUENCE LISTING

<110> Davis, S. Christopher  
 Grate, John H.  
 Gray, David R.  
 Gruber, John M.  
 Huisman, Gjalt W.  
 Ma, Steven K.  
 Newman, Lisa M. Sheldon, Roger  
 Wang, Li A.

<120> Enzymatic Processes for the Production  
 of 4-Substituted 3-Hydroxybutyric Acid Derivatives and  
 Vicinal Cyano, Hydroxy-substituted Carboxylic Acid Esters

<130> 0339.310US

<150> US 10/639,159

<151> 2003-08-11

<150> US 60/402,436

<151> 2002-08-09

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<213> Artificial Sequence

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 KRED CR2-5

<221> CDS

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cat aca aag aat gag agc tta caa gta tta gat tta ttt aag tta aat	96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn	
20 25 30	

gga aaa gta gca agc ata aca gga agc agc agc gga ata gga tat gca	144
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala	
35 40 45	

tta gca gag gct ttt gca caa gtc gga gca gat gta gca ata tgg tat	192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr	

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aat agc cat gat gca aca gga aaa gca gag gca tta gca aag aag tat			240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr			
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gga gta aag gta aag gca tat aaa gca aat gta agc agc agc gat gca			288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala			
	85	90	95
gtc aag caa aca ata gag caa caa ata aag gat ttt gga cat tta gat			336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp			
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Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile			
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Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu			
	145	150	155
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Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser			
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Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn			
	180	185	190
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Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu			
	195	200	205
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Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn			
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	225	230	235
agc tta gtc ccc tta gga agg gga gga gag aca gca gag tta gta gga			768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly			
	245	250	255
gca tat tta ttc tta gca agc gat gca gga agc tat gca aca gga aca			816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr			
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 35 40 45  
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 50 55 60  
 Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr  
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 Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala  
 85 90 95  
 Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp  
 100 105 110  
 Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile  
 115 120 125  
 Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu  
 130 135 140  
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 145 150 155 160  
 Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser  
 165 170 175  
 Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn  
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 Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu  
 195 200 205  
 Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn  
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 Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp  
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cat aca aag aat gag agc tta caa gta tta gat tta ttt aag tta aat	96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn	
20 25 30	
gga aaa gta gca agc ata aca gga agc agc agc gga ata gga tat gca	144
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala	
35 40 45	
tta gca gag gct ttt gca caa gtc gga gca gat gta gca ata tgg tat	192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr	
50 55 60	
aat agc cat gat gca aca gga aaa gca gag gca tta gca aag aag tat	240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr	
65 70 75 80	
gga gta aag gta aag gca tat aaa gca aat gta agc agc agc gat gca	288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala	
85 90 95	
gtc aag caa aca ata gag caa caa ata aag gat ttt gga cat tta gat	336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp	
100 105 110	
ata gta gca gca aat gca gga ata ccc tgg aca aag gga gca tat ata	384
Ile Val Ala Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile	
115 120 125	
gat caa gat gat gac aag cat ttt gac caa gta gta gat gta gac tta	432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu	
130 135 140	
aag gga gta gga tac gta gca aag cat gca gga agg cat ttt agg gaa	480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu	
145 150 155 160	
agg ttt gag aaa gag gga aaa aag gga gca tta gta ttt aca gca agc	528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser	
165 170 175	
atg agc gga cat ata gta aat gtc ccc caa ttc caa gca aca tat aat	576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn	
180 185 190	
gca gca aag gca gga gta agg cat ttt gca aag agc tta gca gtc gag	624
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu	
195 200 205	
ttt gca ccc ttt gca agg gta aat agc gta agc ccc gga tat ata aat	672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn	
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 His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn  
 20 25 30  
 gga aaa gta gca agc ata aca gga agc agc agc gga ata gga tat gca 144  
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 Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr  
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 gga gta aag gta aag gca tat aaa gca aat gta agc agc agc gat gca 288  
 Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala  
 85 90 95  
 gtc aag caa aca ata gag caa caa ata aag gat ttt gga cat tta gat 336  
 Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp  
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 ata gta gta gca aat gca gga ata ccc tgg aca aag gga gca tat ata 384  
 Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile  
 115 120 125  
 gat caa gat gat gac aag cat ttt gac caa gta gta gat gta gac tta 432  
 Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu  
 130 135 140  
 aag gga gta gga tac gta gca aag cat gca gga agg cat ttt agg gaa 480  
 Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu  
 145 150 155 160  
 agg ttt gag aaa gag gga aaa aag gga gca tta gta ttt aca gca agc 528

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			180					185					190				
gca	gca	aag	gca	gga	gta	agg	cat	ttt	gca	aag	agc	tta	gca	gtc	gag		624
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Phe	Ala	Pro	Phe	Ala	Arg	Val	Asn	Ser	Val	Ser	Pro	Gly	Tyr	Ile	Asn		
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Ser	Leu	Val	Pro	Leu	Gly	Arg	Gly	Gly	Glu	Thr	Ala	Glu	Leu	Val	Gly		
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gca	tat	tta	ttc	tta	gca	agc	gat	gca	gga	agc	tat	gca	aca	gga	aca		816
Ala	Tyr	Leu	Phe	Leu	Ala	Ser	Asp	Ala	Gly	Ser	Tyr	Ala	Thr	Gly	Thr		
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Asp	Ile	Ile	Val	Asp	Gly	Gly	Tyr	Thr	Leu	Pro	*						
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Leu	Ala	Glu	Ala	Phe	Ala	Gln	Val	Gly	Ala	Asp	Val	Ala	Ile	Trp	Tyr		
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Asn	Ser	His	Asp	Ala	Thr	Gly	Lys	Ala	Glu	Ala	Leu	Ala	Lys	Lys	Tyr		
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Gly	Val	Lys	Val	Lys	Ala	Tyr	Lys	Ala	Asn	Val	Ser	Ser	Ser	Asp	Ala		
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Val	Lys	Gln	Thr	Ile	Glu	Gln	Gln	Ile	Lys	Asp	Phe	Gly	His	Leu	Asp		
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		115				120						125					
Asp	Gln	Asp	Asp	Asp	Lys	His	Phe	Asp	Gln	Val	Val	Asp	Val	Asp	Leu		
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Lys	Gly	Val	Gly	Tyr	Val	Ala	Lys	His	Ala	Gly	Arg	His	Phe	Arg	Glu		

145		150		155		160									
Arg	Phe	Glu	Lys	Glu	Gly	Lys	Lys	Gly	Ala	Leu	Val	Phe	Thr	Ala	Ser
		165						170						175	
Met	Ser	Gly	His	Ile	Val	Asn	Val	Pro	Gln	Phe	Gln	Ala	Thr	Tyr	Asn
		180						185					190		
Ala	Ala	Lys	Ala	Gly	Val	Arg	His	Phe	Ala	Lys	Ser	Leu	Ala	Val	Glu
		195						200				205			
Phe	Ala	Pro	Phe	Ala	Arg	Val	Asn	Ser	Val	Ser	Pro	Gly	Tyr	Ile	Asn
		210				215				220					
Thr	Glu	Ile	Ser	Asp	Phe	Val	Pro	Gln	Glu	Thr	Gln	Asn	Lys	Trp	Trp
225				230					235					240	
Ser	Leu	Val	Pro	Leu	Gly	Arg	Gly	Gly	Glu	Thr	Ala	Glu	Leu	Val	Gly
		245						250				255			
Ala	Tyr	Leu	Phe	Leu	Ala	Ser	Asp	Ala	Gly	Ser	Tyr	Ala	Thr	Gly	Thr
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cat aca aag aat gag agc tta caa gta tta gat tta ttt aag tta aat	96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn	
20 25 30	
gga aaa gta gca agc ata aca gga agc agc agc gga ata gga tat gca	144
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala	
35 40 45	
tta gca gag gct ttt gca caa gtc gga gca gat gta gca ata tgg tat	192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr	
50 55 60	
aat agc cat gat gca aca gga aaa gca gag gca tta gca aag aag tat	240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr	
65 70 75 80	
gga gta aag gta aag gca tat aaa gca aat gta agc agc agc gat gca	288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala	
85 90 95	
gtc aag caa aca ata gag caa caa ata aag gat ttt gga cat tta gat	336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp	



100	105	110	
ata gta gta gca aat gca gga	ata ccc tgg aca aag gga gca tat ata		384
Ile Val Val Ala Asn Ala Gly	Ile Pro Trp Thr Lys Gly Ala Tyr Ile		
115	120	125	
gat caa gat gat gac aag cat ttt gac caa gta gta gat gta gac tta			432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu			
130	135	140	
aag gga gta gga tac gta gca aag cat gca gga agg cat ttt agg gaa			480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu			
145	150	155	160
agg ttt gag aaa gag gga aaa aag gga gca tta gta ttt aca gca agc			528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser			
165	170	175	
atg agc gga cat ata gta aat gtc ccc caa ttc caa gca aca tat aat			576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn			
180	185	190	
gca gca aag gca gga gta agg cat ttt gca aag agc tta gca gtc gag			624
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu			
195	200	205	
ttt gca ccc ttt gca agg gta aat agc gta agc ccc gga tat ata aat			672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn			
210	215	220	
aca gag ata agc gat ttc gtc ccc caa gag aca caa aat aag tgg tgg			720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp			
225	230	235	240
agc tta gtc ccc tta gga agg gga gga gag aca gca gag tta gta gga			768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly			
245	250	255	
gca tat tta ttc tta gca agc gat gca gga agc tat gca aca gga aca			816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr			
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 <213> Candida magnoliae

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 35 40 45  
 Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr  
 50 55 60  
 Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr  
 65 70 75 80  
 Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala  
 85 90 95  
 Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp  
 100 105 110  
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 115 120 125  
 Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu  
 130 135 140  
 Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu  
 145 150 155 160  
 Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser  
 165 170 175  
 Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn  
 180 185 190  
 Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu  
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 Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn  
 210 215 220  
 Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp  
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 Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly  
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 Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala  
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 Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val  
 35 40 45  
 aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc gtc caa gga 192

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Asp	Val	Thr	Lys	Glu	Glu	Asp	Val	Lys	Asn	Ile	Val	Gln	Thr	Ala	Ile		
65					70					75					80		
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Lys	Glu	Phe	Gly	Thr	Leu	Asp	Ile	Met	Ile	Asn	Asn	Ala	Gly	Leu	Glu		
				85					90					95			
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Asn	Pro	Val	Pro	Ser	His	Glu	Met	Pro	Leu	Lys	Asp	Trp	Asp	Lys	Val		
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atc	ggc	acg	aac	tta	acg	ggg	gcc	ttt	tta	gga	agc	cgt	gaa	gcg	att	384	
Ile	Gly	Thr	Asn	Leu	Thr	Gly	Ala	Phe	Leu	Gly	Ser	Arg	Glu	Ala	Ile		
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aaa	tat	ttc	gta	gaa	aac	gat	atc	aag	gga	aat	gtc	att	aac	atg	tcc	432	
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Ser	Val	His	Glu	Val	Ile	Pro	Trp	Pro	Leu	Phe	Val	His	Tyr	Ala	Ala		
	145				150					155					160		
agt	aaa	ggc	ggg	ata	aag	ctg	atg	aca	gaa	aca	tta	gcg	ttg	gaa	tac	528	
Ser	Lys	Gly	Gly	Ile	Lys	Leu	Met	Thr	Glu	Thr	Leu	Ala	Leu	Glu	Tyr		
				165					170					175			
gcg	ccg	aag	ggc	att	cgc	gtc	aat	aat	att	ggg	cca	ggg	gcg	atc	aac	576	
Ala	Pro	Lys	Gly	Ile	Arg	Val	Asn	Asn	Ile	Gly	Pro	Gly	Ala	Ile	Asn		
			180					185					190				
acg	cca	atc	aat	gct	gaa	aaa	ttc	gct	gac	cct	aaa	cag	aaa	gct	gat	624	
Thr	Pro	Ile	Asn	Ala	Glu	Lys	Phe	Ala	Asp	Pro	Lys	Gln	Lys	Ala	Asp		
			195				200					205					
gta	gaa	agc	atg	att	cca	atg	gga	tat	atc	ggc	gaa	ccg	gag	gag	atc	672	
Val	Glu	Ser	Met	Ile	Pro	Met	Gly	Tyr	Ile	Gly	Glu	Pro	Glu	Glu	Ile		
	210					215					220						
gcc	gca	gta	gca	gcc	tgg	ctt	gct	tcg	aag	gaa	gcc	agc	tac	gtc	aca	720	
Ala	Ala	Val	Ala	Ala	Trp	Leu	Ala	Ser	Lys	Glu	Ala	Ser	Tyr	Val	Thr		
	225				230					235				240			
ggc	atc	acg	tta	ttc	gcg	gac	ggc	ggg	atg	aca	caa	tat	cct	tca	ttc	768	
Gly	Ile	Thr	Leu	Phe	Ala	Asp	Gly	Gly	Met	Thr	Gln	Tyr	Pro	Ser	Phe		
			245					250						255			
cag	gca	ggc	cgc	ggg	taa											786	
Gln	Ala	Gly	Arg	Gly	*												
			260														

<210> 10

<211> 261  
 <212> PRT  
 <213> Bacillus sp.

<400> 10

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Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
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Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
20        25        30
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
35        40        45
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Gln Gly
50        55        60
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
65        70        75        80
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
85        90        95
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
100       105       110
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
115       120       125
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
130       135       140
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
145       150       155       160
Ser Lys Gly Gly Ile Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
165       170       175
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
180       185       190
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp
195       200       205
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
210       215       220
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr
225       230       235       240
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
245       250       255
Gln Ala Gly Arg Gly
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<210> 11  
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 <212> DNA  
 <213> Bacillus sp.

<220>

<221> CDS

<222> (1)...(786)

<223> Glucose dehydrogenase M02-6

<400> 11

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Met Tyr Lys Asp Leu Glu Gly Lys Val Val Val Ile Thr Gly Ser Ser
1          5          10          15

acc ggt tta gga aaa gca atg gcg att cgt ttt gcg aca gaa aaa gct      96
Thr Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Ala Thr Glu Lys Ala

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20	25	30	
aaa gta gtt gtg aat tat cgt tcg	aaa gaa gaa gaa gct aac agc gtt	144	
Lys Val Val Val Asn Tyr Arg Ser	Lys Glu Glu Glu Ala Asn Ser Val		
35	40 45		
tta gaa gaa att aaa aaa gtc ggc gga gag gca att gcg gtt aaa ggt	192		
Leu Glu Glu Ile Lys Lys Val Gly Gly Glu Ala Ile Ala Val Lys Gly			
50 55 60			
gac gta aca gtt gag tct gac gtg atc aat tta gtt caa tct gct att	240		
Asp Val Thr Val Glu Ser Asp Val Ile Asn Leu Val Gln Ser Ala Ile			
65 70 75 80			
aaa gaa ttt gga aag tta gat gtt atg att aat aac gca gga atg gaa	288		
Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu			
85 90 95			
aat ccg gtt tca tct cat gaa atg tct tta agc gat tgg aat aaa gta	336		
Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val			
100 105 110			
att gat acg aac tta acg gga gca ttt tta gga agc cgt gaa gcg att	384		
Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile			
115 120 125			
aaa tat ttc gtg gaa aat gat att aag gga aca gtt att aat atg tcg	432		
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Thr Val Ile Asn Met Ser			
130 135 140			
agt gtt cat gag aaa att cct tgg cca tta ttt gtt cat tac gca gca	480		
Ser Val His Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala			
145 150 155 160			
agt aaa ggt ggc atg aag ctc atg act gaa aca ctt gca tta gaa tat	528		
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr			
165 170 175			
gct cca aaa ggt att cgt gta aat aac att ggg ccg gga gcg att aat	576		
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn			
180 185 190			
aca ccg att aac gct gag aaa ttt gct gat cct aag cag cgc gca gat	624		
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Arg Ala Asp			
195 200 205			
gta gaa agc atg att cca atg gga tac atc gga gag ccg gaa gaa att	672		
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile			
210 215 220			
gca gcg gtt gct gca tgg cta gct tct tca gaa gca agt tat gta aca	720		
Ala Ala Val Ala Ala Trp Leu Ala Ser Ser Glu Ala Ser Tyr Val Thr			
225 230 235 240			
ggg att acg ctc ttt gct gac ggc ggt atg aca cag tac cca tca ttc	768		
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe			
245 250 255			

caa gca gga cgc gga taa  
 Gln Ala Gly Arg Gly \*  
 260

786

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 <211> 261  
 <212> PRT  
 <213> Bacillus sp.

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 20 25 30  
 Lys Val Val Val Asn Tyr Arg Ser Lys Glu Glu Glu Ala Asn Ser Val  
 35 40 45  
 Leu Glu Glu Ile Lys Lys Val Gly Gly Glu Ala Ile Ala Val Lys Gly  
 50 55 60  
 Asp Val Thr Val Glu Ser Asp Val Ile Asn Leu Val Gln Ser Ala Ile  
 65 70 75 80  
 Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu  
 85 90 95  
 Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val  
 100 105 110  
 Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile  
 115 120 125  
 Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Thr Val Ile Asn Met Ser  
 130 135 140  
 Ser Val His Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala  
 145 150 155 160  
 Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr  
 165 170 175  
 Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn  
 180 185 190  
 Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Arg Ala Asp  
 195 200 205  
 Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile  
 210 215 220  
 Ala Ala Val Ala Ala Trp Leu Ala Ser Ser Glu Ala Ser Tyr Val Thr  
 225 230 235 240  
 Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe  
 245 250 255  
 Gln Ala Gly Arg Gly  
 260

<210> 13  
 <211> 765  
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 <213> Artificial Sequence

<220>  
 <223> HHDH.1

<221> CDS  
 <222> (1)...(765)

<400> 13

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agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat	96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	
gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac	144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa	192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat	288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
ttc atc act tcg gct act ccg ttc ggg ccg tgg aag gag cta tcg act	432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg	480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser	
145 150 155 160	
aag gag cta ggg gag tac aat atc ccg gtg ttc gct atc ggg ccg aat	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp	
180 185 190	
aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta	624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg	672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu	
210 215 220	

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca 720  
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala  
 225 230 235 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa 765  
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu \*  
 245 250

<210> 14  
 <211> 254  
 <212> PRT  
 <213> Agrobacterium sp.

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 20 25 30  
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr  
 35 40 45  
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu  
 50 55 60  
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp  
 65 70 75 80  
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp  
 85 90 95  
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val  
 100 105 110  
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile  
 115 120 125  
 Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr  
 130 135 140  
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser  
 145 150 155 160  
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn  
 165 170 175  
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp  
 180 185 190  
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu  
 195 200 205  
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu  
 210 215 220  
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala  
 225 230 235 240  
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  
 245 250

<210> 15  
 <211> 765  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HHDH.2



<221> CDS

<222> (1)...(765)

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1 5 10 15	

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat	96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac	144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa	192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	

gct gtc acc agc gct tac ggt caa gtc gat gtc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat	288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	

ttc atc act tcg gct act ccg ttc ggg ccg tgg aag gag cta tcg act	432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	

tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg	480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser	
145 150 155 160	

aag gag cta ggg gag tac aat atc ccg gtg ttc gct atc ggg ccg aat	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp	
180 185 190	

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta	624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	

caa cga tta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg	672
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Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu  
 210 215 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca 720  
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala  
 225 230 235 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa 765  
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu \*  
 245 250

<210> 16  
 <211> 254  
 <212> PRT  
 <213> Agrobacterium sp.

<400> 16  
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 20 25 30  
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr  
 35 40 45  
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu  
 50 55 60  
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp  
 65 70 75 80  
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp  
 85 90 95  
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val  
 100 105 110  
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile  
 115 120 125  
 Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr  
 130 135 140  
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser  
 145 150 155 160  
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn  
 165 170 175  
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp  
 180 185 190  
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu  
 195 200 205  
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu  
 210 215 220  
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala  
 225 230 235 240  
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  
 245 250

<210> 17  
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<220>

<223> HHDH.16

<221> CDS

<222> (1)...(765)

<400> 17

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1				5					10					15		

agc	gct	ctg	agg	ctg	agc	gaa	gct	ggg	cat	acc	gtc	gct	tgc	cat	gat	96
Ser	Ala	Leu	Arg	Leu	Ser	Glu	Ala	Gly	His	Thr	Val	Ala	Cys	His	Asp	
		20					25						30			

gaa	agc	ttt	aaa	cag	aaa	gat	gaa	ctg	gaa	gct	ttt	gct	gaa	acc	tac	144
Glu	Ser	Phe	Lys	Gln	Lys	Asp	Glu	Leu	Glu	Ala	Phe	Ala	Glu	Thr	Tyr	
		35					40					45				

cca	cag	ctg	aaa	cca	atg	agc	gaa	cag	gaa	cca	gct	gaa	ctg	atc	gaa	192
Pro	Gln	Leu	Lys	Pro	Met	Ser	Glu	Gln	Glu	Pro	Ala	Glu	Leu	Ile	Glu	
	50					55					60					

gct	gtc	acc	agc	gct	tac	ggg	cag	gtc	gat	gtc	ctg	gtc	agc	aac	gat	240
Ala	Val	Thr	Ser	Ala	Tyr	Gly	Gln	Val	Asp	Val	Leu	Val	Ser	Asn	Asp	
65					70				75						80	

atc	ttt	gct	cca	gaa	ttt	cag	cca	atc	gat	aaa	tac	gct	gtc	gaa	gat	288
Ile	Phe	Ala	Pro	Glu	Phe	Gln	Pro	Ile	Asp	Lys	Tyr	Ala	Val	Glu	Asp	
				85					90					95		

tac	agg	ggg	gct	gtc	gaa	gct	ctg	cag	atc	agg	cca	ttt	gct	cta	gtg	336
Tyr	Arg	Gly	Ala	Val	Glu	Ala	Leu	Gln	Ile	Arg	Pro	Phe	Ala	Leu	Val	
			100					105					110			

aat	gct	gtg	gct	tcg	caa	atg	aag	aag	cga	aag	tcg	ggg	cac	atc	atc	384
Asn	Ala	Val	Ala	Ser	Gln	Met	Lys	Lys	Arg	Lys	Ser	Gly	His	Ile	Ile	
		115					120					125				

ttc	atc	act	tcg	gct	act	ccg	ttc	ggg	ccg	tgg	aag	gag	cta	tcg	act	432
Phe	Ile	Thr	Ser	Ala	Thr	Pro	Phe	Gly	Pro	Trp	Lys	Glu	Leu	Ser	Thr	
	130					135					140					

tac	act	tcg	gct	cga	gct	ggg	gct	tgt	act	cta	gct	aat	gct	cta	tcg	480
Tyr	Thr	Ser	Ala	Arg	Ala	Gly	Ala	Cys	Thr	Leu	Ala	Asn	Ala	Leu	Ser	
145					150					155					160	

aag	gag	cta	gga	gag	tac	aat	atc	ccg	gtg	ttc	gct	atc	ggg	ccg	aat	528
Lys	Glu	Leu	Gly	Glu	Tyr	Asn	Ile	Pro	Val	Phe	Ala	Ile	Gly	Pro	Asn	
			165						170					175		

tac	cta	cac	tcg	gag	gat	tcg	ccg	tac	ttc	tac	ccg	act	gag	ccg	tgg	576
Tyr	Leu	His	Ser	Glu	Asp	Ser	Pro	Tyr	Phe	Tyr	Pro	Thr	Glu	Pro	Trp	
			180					185					190			

aag	act	aat	ccg	gag	cac	gtg	gct	cac	gtg	aag	aag	gtg	act	gct	cta	624
Lys	Thr	Asn	Pro	Glu	His	Val	Ala	His	Val	Lys	Lys	Val	Thr	Ala	Leu	
		195					200								205	

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg	672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu	
210 215 220	

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca	720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala	
225 230 235 240	

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa	765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *	
245 250	

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 <211> 254  
 <212> PRT  
 <213> Agrobacterium sp.

<400> 18	
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20 25 30	
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser	
145 150 155 160	
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp	
180 185 190	
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu	
210 215 220	
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala	
225 230 235 240	
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu	
245 250	

<210> 19  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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 <210> 20  
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 <212> DNA  
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 gaattcgccc atatgtataa agatttagaa gg 32  
  
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 ggccggatcc tcattatccg cgtcctgctt gga 33  
  
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 <212> DNA  
 <213> Artificial Sequence  
  
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 <221> CDS  
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 Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly  
 1 5 10 15  
  
 agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat 96

Ser	Ala	Leu	Arg	Leu	Ser	Glu	Ala	Gly	His	Thr	Val	Ala	Cys	His	Asp	
			20					25					30			
gaa	agc	ttt	aaa	cag	aaa	gat	gaa	ctg	gaa	gct	ttt	gct	gaa	acc	tac	144
Glu	Ser	Phe	Lys	Gln	Lys	Asp	Glu	Leu	Glu	Ala	Phe	Ala	Glu	Thr	Tyr	
		35					40					45				
cca	cag	ctg	aaa	cca	atg	agc	gaa	cag	gaa	cca	gct	gaa	ctg	atc	gaa	192
Pro	Gln	Leu	Lys	Pro	Met	Ser	Glu	Gln	Glu	Pro	Ala	Glu	Leu	Ile	Glu	
		50				55					60					
gct	gtc	acc	agc	gct	tac	ggg	cag	gtc	gat	gtc	ctg	gtc	agc	aac	gat	240
Ala	Val	Thr	Ser	Ala	Tyr	Gly	Gln	Val	Asp	Val	Leu	Val	Ser	Asn	Asp	
		65			70				75						80	
atc	ttt	gct	cca	gaa	ttt	cag	cca	atc	gat	aaa	tac	gct	gtc	gaa	gat	288
Ile	Phe	Ala	Pro	Glu	Phe	Gln	Pro	Ile	Asp	Lys	Tyr	Ala	Val	Glu	Asp	
			85					90						95		
tac	agg	ggg	gct	gtc	gaa	gct	ctg	cag	atc	agg	cca	ttt	gct	cta	gtg	336
Tyr	Arg	Gly	Ala	Val	Glu	Ala	Leu	Gln	Ile	Arg	Pro	Phe	Ala	Leu	Val	
			100				105					110				
aat	gct	gtg	gct	tcg	caa	atg	aag	aag	cga	aag	tcg	ggg	cac	atc	atc	384
Asn	Ala	Val	Ala	Ser	Gln	Met	Lys	Lys	Arg	Lys	Ser	Gly	His	Ile	Ile	
		115				120					125					
ttc	atc	act	tcg	gct	gct	ccg	ttc	ggg	cca	tgg	aaa	gag	cta	tcg	act	432
Phe	Ile	Thr	Ser	Ala	Ala	Pro	Phe	Gly	Pro	Trp	Lys	Glu	Leu	Ser	Thr	
		130				135				140						
tac	act	tcg	gct	cga	gct	ggg	gct	tgt	act	cta	gct	aat	gct	cta	tcg	480
Tyr	Thr	Ser	Ala	Arg	Ala	Gly	Ala	Cys	Thr	Leu	Ala	Asn	Ala	Leu	Ser	
		145			150				155					160		
aag	gag	cta	gga	gag	tac	aat	atc	ccg	gtg	ttc	gct	atc	ggg	ccg	aat	528
Lys	Glu	Leu	Gly	Glu	Tyr	Asn	Ile	Pro	Val	Phe	Ala	Ile	Gly	Pro	Asn	
			165					170					175			
tac	cta	cac	tcg	gag	gat	tcg	ccg	tac	ttc	tac	ccg	act	gag	ccg	tgg	576
Tyr	Leu	His	Ser	Glu	Asp	Ser	Pro	Tyr	Phe	Tyr	Pro	Thr	Glu	Pro	Trp	
			180				185					190				
aag	act	aat	ccg	gag	cac	gtg	gct	cac	gtg	aag	aag	gtg	act	gct	cta	624
Lys	Thr	Asn	Pro	Glu	His	Val	Ala	His	Val	Lys	Lys	Val	Thr	Ala	Leu	
		195				200					205					
caa	cga	cta	ggg	act	caa	aaa	gag	ttg	ggg	gaa	ttg	gtg	gca	ttc	ttg	672
Gln	Arg	Leu	Gly	Thr	Gln	Lys	Glu	Leu	Gly	Glu	Leu	Val	Ala	Phe	Leu	
		210				215					220					
gca	tct	ggc	tct	tgt	gat	tat	ttg	act	ggc	cag	gtg	ttt	tgg	ttg	gca	720
Ala	Ser	Gly	Ser	Cys	Asp	Tyr	Leu	Thr	Gly	Gln	Val	Phe	Trp	Leu	Ala	
		225			230				235					240		
ggc	ggc	ttt	ccc	atg	ata	gaa	cgt	tgg	ccc	ggc	atg	ccc	gaa	taa		765
Gly	Gly	Phe	Pro	Met	Ile	Glu	Arg	Trp	Pro	Gly	Met	Pro	Glu	*		

245

250

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 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HHDH P016013-B-03

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 20 25 30  
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr  
 35 40 45  
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu  
 50 55 60  
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp  
 65 70 75 80  
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp  
 85 90 95  
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val  
 100 105 110  
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile  
 115 120 125  
 Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr  
 130 135 140  
 Tyr Thr Ser Ala Arg Ala Cys Thr Leu Ala Asn Ala Leu Ser  
 145 150 155 160  
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn  
 165 170 175  
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp  
 180 185 190  
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu  
 195 200 205  
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu  
 210 215 220  
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala  
 225 230 235 240  
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  
 245 250

<210> 25  
 <211> 765  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HHDH P016015-C-04

<221> CDS  
 <222> (1)...(765)

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agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat	96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	
gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac	144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa	192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc cag gat	288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp	
85 90 95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct ctg gcg	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Ala	
100 105 110	
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
ttc atc act tcg gct gct ccg ttc ggg cca tgg aag gag cta tcg act	432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg	480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser	
145 150 155 160	
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp	
180 185 190	
aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta	624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg	672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu	
210 215 220	
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca	720



Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala  
 225 230 235 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa 765  
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu \*  
 245 250

<210> 26  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HHDH P016015-C-04

<400> 26  
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 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr  
 35 40 45  
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu  
 50 55 60  
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp  
 65 70 75 80  
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp  
 85 90 95  
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Ala  
 100 105 110  
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile  
 115 120 125  
 Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr  
 130 135 140  
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser  
 145 150 155 160  
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn  
 165 170 175  
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp  
 180 185 190  
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu  
 195 200 205  
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu  
 210 215 220  
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala  
 225 230 235 240  
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  
 245 250

<210> 27  
 <211> 765  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HHDH P016014-E-01

<221> CDS

<222> (1)...(765)

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1 5 10 15	
agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat	96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	
gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac	144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gac ctg att gaa	192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Asp Leu Ile Glu	
50 55 60	
gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gac	288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
aat gct gtg gct tcg caa atg aag aaa cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
ttc atc act tcg gct act ccg ttc ggg cca tgg aaa gag cta tcg act	432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg	480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser	
145 150 155 160	
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp	
180 185 190	
aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta	624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttc ctg 672  
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu  
 210 215 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca 720  
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala  
 225 230 235 240

ggc ggc ttt ccc att ata gaa cgt tgg ccc ggc atg ccc gaa taa 765  
 Gly Gly Phe Pro Ile Ile Glu Arg Trp Pro Gly Met Pro Glu \*  
 245 250

<210> 28  
 <211> 254  
 <212> PRT  
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<220>  
 <223> HHDH P016014-E-01

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 20 25 30  
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr  
 35 40 45  
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Asp Leu Ile Glu  
 50 55 60  
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp  
 65 70 75 80  
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp  
 85 90 95  
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val  
 100 105 110  
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile  
 115 120 125  
 Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr  
 130 135 140  
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser  
 145 150 155 160  
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn  
 165 170 175  
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp  
 180 185 190  
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu  
 195 200 205  
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu  
 210 215 220  
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala  
 225 230 235 240  
 Gly Gly Phe Pro Ile Ile Glu Arg Trp Pro Gly Met Pro Glu  
 245 250

<210> 29  
 <211> 768

<212> DNA

<213> Artificial Sequence

<220>

<223> HHDH P016014-G-08

<221> CDS

<222> (1)...(765)

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1				5					10					15		

agc	gct	ctg	aaa	ctg	agc	gaa	gct	ggt	cat	acc	gtc	gct	tgc	cat	gat	96
Ser	Ala	Leu	Lys	Leu	Ser	Glu	Ala	Gly	His	Thr	Val	Ala	Cys	His	Asp	
			20					25					30			

ggt	agc	ttt	aag	cat	aaa	gat	gaa	ctg	gaa	gct	ttt	gct	gaa	gcc	tac	144
Gly	Ser	Phe	Lys	His	Lys	Asp	Glu	Leu	Glu	Ala	Phe	Ala	Glu	Ala	Tyr	
		35					40					45				

cca	cag	ctg	aaa	cca	atg	agc	gaa	cag	gaa	cca	gct	gaa	ctg	att	gaa	192
Pro	Gln	Leu	Lys	Pro	Met	Ser	Glu	Gln	Glu	Pro	Ala	Glu	Leu	Ile	Glu	
	50					55					60					

gct	gtc	acc	agc	gct	ttt	ggt	cat	gtc	gat	gtc	ctg	gtc	agc	aac	gat	240
Ala	Val	Thr	Ser	Ala	Phe	Gly	His	Val	Asp	Val	Leu	Val	Ser	Asn	Asp	
65					70				75					80		

atc	ttt	gct	cta	gaa	ttt	cgg	cca	atc	gat	aaa	tac	gct	gtc	gag	gat	288
Ile	Phe	Ala	Leu	Glu	Phe	Arg	Pro	Ile	Asp	Lys	Tyr	Ala	Val	Glu	Asp	
				85					90					95		

tac	agg	ggt	gct	gtc	gaa	gct	ctg	cag	atc	agg	cca	ttt	gct	cta	gtg	336
Tyr	Arg	Gly	Ala	Val	Glu	Ala	Leu	Gln	Ile	Arg	Pro	Phe	Ala	Leu	Val	
			100					105					110			

aat	gct	gtg	gct	cca	caa	atg	aag	aag	cga	aag	tcg	ggg	cac	atc	atc	384
Asn	Ala	Val	Ala	Pro	Gln	Met	Lys	Lys	Arg	Lys	Ser	Gly	His	Ile	Ile	
		115					120					125				

ttc	atc	act	tcg	gct	gcc	ccg	ttc	ggg	cca	tgg	aag	gag	cta	tcg	act	432
Phe	Ile	Thr	Ser	Ala	Ala	Pro	Phe	Gly	Pro	Trp	Lys	Glu	Leu	Ser	Thr	
		130				135					140					

tac	tct	tcg	gct	cga	gct	ggg	gct	agt	gca	cta	gct	aat	gct	cta	tcg	480
Tyr	Ser	Ser	Ala	Arg	Ala	Gly	Ala	Ser	Ala	Leu	Ala	Asn	Ala	Leu	Ser	
145					150					155				160		

aag	gag	cta	gga	gag	tac	aat	atc	ccg	gtg	ttc	gct	atc	ggg	ccg	aat	528
Lys	Glu	Leu	Gly	Glu	Tyr	Asn	Ile	Pro	Val	Phe	Ala	Ile	Gly	Pro	Asn	
			165						170					175		

tac	cta	cac	tcg	gag	gat	tcg	ccg	ttc	tat	tac	ccc	act	gag	ccg	tgg	576
Tyr	Leu	His	Ser	Glu	Asp	Ser	Pro	Phe	Tyr	Tyr	Pro	Thr	Glu	Pro	Trp	
			180					185					190			

aag att aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta	624
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg	672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu	
210 215 220	

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca	720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala	
225 230 235 240	

ggc ggc ttt ccc gct ata gaa cgt tgg ccc ggc atg ccc gaa taa	765
Gly Gly Phe Pro Ala Ile Glu Arg Trp Pro Gly Met Pro Glu *	
245 250	

tga	768
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<210> 30  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HHDH P016014-G-08

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20 25 30	
Gly Ser Phe Lys His Lys Asp Glu Leu Glu Ala Phe Ala Glu Ala Tyr	
35 40 45	
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
Ala Val Thr Ser Ala Phe Gly His Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
Ile Phe Ala Leu Glu Phe Arg Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
Asn Ala Val Ala Pro Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
Tyr Ser Ser Ala Arg Ala Gly Ala Ser Ala Leu Ala Asn Ala Leu Ser	
145 150 155 160	
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
Tyr Leu His Ser Glu Asp Ser Pro Phe Tyr Tyr Pro Thr Glu Pro Trp	
180 185 190	
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu	
210 215 220	
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala	



Lys	Glu	Leu	Gly	Glu	Tyr	Asn	Ile	Pro	Val	Phe	Ala	Ile	Gly	Pro	Asn		
			165						170					175			
tac	cta	cac	tcg	gag	gat	tcg	ccg	tac	ttc	tac	ccg	act	gag	ccg	tgg	576	
Tyr	Leu	His	Ser	Glu	Asp	Ser	Pro	Tyr	Phe	Tyr	Pro	Thr	Glu	Pro	Trp		
			180					185					190				
aag	act	aat	ccg	gag	cac	gtg	gct	cac	gtg	aag	aag	gtg	act	gct	cta	624	
Lys	Thr	Asn	Pro	Glu	His	Val	Ala	His	Val	Lys	Lys	Val	Thr	Ala	Leu		
			195				200					205					
caa	cga	cta	ggg	act	caa	aaa	gag	ttg	ggg	gaa	ttg	gtg	gca	ttt	ttg	672	
Gln	Arg	Leu	Gly	Thr	Gln	Lys	Glu	Leu	Gly	Glu	Leu	Val	Ala	Phe	Leu		
	210					215					220						
gca	tct	ggc	tct	tgt	gat	tat	ttg	act	ggc	cag	gtg	ttt	tgg	ttg	gca	720	
Ala	Ser	Gly	Ser	Cys	Asp	Tyr	Leu	Thr	Gly	Gln	Val	Phe	Trp	Leu	Ala		
225					230				235					240			
ggc	ggc	ttt	ccc	atg	ata	gaa	cgt	tgg	ccc	ggc	atg	ccc	gaa	taa		765	
Gly	Gly	Phe	Pro	Met	Ile	Glu	Arg	Trp	Pro	Gly	Met	Pro	Glu	*			
			245					250									

<210> 32  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HHDH Mz1/2G5

<400> 32

Met	Ser	Thr	Ala	Ile	Val	Thr	Asn	Val	Lys	His	Phe	Gly	Gly	Met	Gly		
1				5					10					15			
Ser	Ala	Leu	Arg	Leu	Ser	Glu	Ala	Gly	His	Thr	Val	Ala	Cys	His	Asp		
		20						25					30				
Glu	Ser	Phe	Lys	Gln	Lys	Asp	Glu	Leu	Glu	Ala	Phe	Ala	Glu	Thr	Tyr		
		35				40					45						
Pro	Gln	Leu	Lys	Pro	Met	Ser	Glu	Gln	Glu	Pro	Ala	Glu	Leu	Ile	Glu		
	50				55					60							
Ala	Val	Thr	Ser	Ala	Tyr	Gly	Gln	Val	Asp	Val	Leu	Val	Ser	Asn	Asp		
65				70					75					80			
Ile	Phe	Ala	Pro	Glu	Phe	Gln	Pro	Ile	Asp	Lys	Tyr	Ala	Val	Glu	Asp		
			85					90					95				
Tyr	Arg	Gly	Ala	Val	Glu	Ala	Leu	Gln	Ile	Arg	Pro	Phe	Ala	Leu	Val		
		100						105					110				
Asn	Ala	Val	Ala	Ser	Gln	Met	Lys	Lys	Arg	Lys	Ser	Gly	His	Ile	Ile		
	115					120						125					
Phe	Ile	Thr	Ser	Ala	Thr	Pro	Phe	Gly	Pro	Trp	Lys	Glu	Leu	Ser	Thr		
	130				135					140							
Tyr	Thr	Ser	Ala	Arg	Ala	Gly	Ala	Cys	Thr	Leu	Ala	Asn	Ala	Leu	Ser		
145				150					155					160			
Lys	Glu	Leu	Gly	Glu	Tyr	Asn	Ile	Pro	Val	Phe	Ala	Ile	Gly	Pro	Asn		
			165					170					175				
Tyr	Leu	His	Ser	Glu	Asp	Ser	Pro	Tyr	Phe	Tyr	Pro	Thr	Glu	Pro	Trp		
			180					185					190				

Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu  
           195                                  200                                  205  
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu  
           210                                  215                                  220  
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala  
 225                                  230                                  235                                  240  
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  
                                   245                                  250

<210> 33  
 <211> 765  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HHDH Mz1.1A5

<221> CDS  
 <222> (1)...(765)

<400> 33  
 atg agc ccc gct atc gtc act aac gtc aaa cat ttt ggt ggt atg ggt 48  
 Met Ser Pro Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly  
   1                                  5                                  10                                  15  
  
 acc gct ctg agg ctg agc gaa gct ggt caa acc gtc gct tgc cat gat 96  
 Thr Ala Leu Arg Leu Ser Glu Ala Gly Gln Thr Val Ala Cys His Asp  
           20                                  25                                  30  
  
 gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac 144  
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr  
           35                                  40                                  45  
  
 cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa 192  
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu  
           50                                  55                                  60  
  
 gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat 240  
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp  
   65                                  70                                  75                                  80  
  
 atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat 288  
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp  
           85                                  90                                  95  
  
 tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg 336  
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val  
           100                                  105                                  110  
  
 aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc 384  
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile  
           115                                  120                                  125  
  
 ttc atc act tcg gct act ccg ttc ggg ccg tgg aag gag cta tcg act 432  
 Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr  
   130                                  135                                  140



tac	act	tcg	gct	cga	gct	ggg	gct	tgt	act	cta	gct	aat	gct	cta	tcg	480
Tyr	Thr	Ser	Ala	Arg	Ala	Gly	Ala	Cys	Thr	Leu	Ala	Asn	Ala	Leu	Ser	
145					150					155					160	

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg 576  
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp  
 180 185 190

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg 672  
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu  
210 215 220

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa 765  
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu \*  
245 250

<220>  
<223> HHDH Mz1.1A5

145		150		155		160									
Lys	Glu	Leu	Gly	Glu	Tyr	Asn	Ile	Pro	Val	Phe	Ala	Ile	Gly	Pro	Asn
			165						170					175	
Tyr	Leu	His	Ser	Glu	Asp	Ser	Pro	Tyr	Phe	Tyr	Pro	Thr	Glu	Pro	Trp
			180						185					190	
Lys	Thr	Asn	Pro	Glu	His	Val	Ala	His	Val	Lys	Lys	Val	Thr	Ala	Leu
		195						200					205		
Gln	Arg	Leu	Gly	Thr	Gln	Lys	Glu	Leu	Gly	Glu	Leu	Val	Ala	Phe	Leu
	210					215					220				
Ala	Ser	Gly	Ser	Cys	Asp	Tyr	Leu	Thr	Gly	Gln	Val	Phe	Trp	Leu	Ala
225					230					235					240
Gly	Gly	Phe	Pro	Met	Ile	Glu	Arg	Trp	Pro	Gly	Met	Pro	Glu		
			245						250						

<210> 35  
 <211> 765  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HHDH cys1.10

<221> CDS  
 <222> (1)...(765)

<400> 35	
atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt	48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly	
1 5 10 15	
agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat	96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	
gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac	144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa	192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat	288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	

ttc atc act tcg gct act ccg ttc ggg cca tgg aag gag cta tcg act	432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
tac act tcg gct cga gct ggg gct agt act cta gct aat gct cta tcg	480
Tyr Thr Ser Ala Arg Ala Gly Ala Ser Thr Leu Ala Asn Ala Leu Ser	
145 150 155 160	
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp	
180 185 190	
aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta	624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg	672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu	
210 215 220	
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca	720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala	
225 230 235 240	
ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa	765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *	
245 250	

<210> 36

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> HHDH cys1.10

<400> 36

Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly	
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Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	

Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile  
           115                          120                          125  
 Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr  
           130                          135                          140  
 Tyr Thr Ser Ala Arg Ala Gly Ala Ser Thr Leu Ala Asn Ala Leu Ser  
 145                          150                          155                          160  
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn  
                           165                          170                          175  
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp  
                           180                          185                          190  
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu  
           195                          200                          205  
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu  
           210                          215                          220  
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala  
 225                          230                          235                          240  
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  
                           245                          250

<210> 37  
 <211> 765  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HHDH cys2.12

<221> CDS  
 <222> (1)...(765)

<400> 37  
 atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt 48  
 Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly  
   1                          5                          10                          15  
  
 agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct gcg cat gat 96  
 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Ala His Asp  
           20                          25                          30  
  
 gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac 144  
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr  
           35                          40                          45  
  
 cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa 192  
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu  
           50                          55                          60  
  
 gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat 240  
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp  
   65                          70                          75                          80  
  
 atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat 288  
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp  
           85                          90                          95  
  
 tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg 336  
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val

100	105	110	
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc			384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile			
115	120	125	
ttc atc act tcg gct act ccg ttc ggg cca tgg aag gag cta tcg act			432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr			
130	135	140	
tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg			480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser			
145	150	155 160	
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat			528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn			
165	170	175	
tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg			576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp			
180	185	190	
aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta			624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu			
195	200	205	
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg			672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu			
210	215	220	
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca			720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala			
225	230	235 240	
ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa			765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *			
245	250		

<210> 38  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HHDH cys2.12

<400> 38  
 Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly  
 1 5 10 15  
 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Ala His Asp  
 20 25 30  
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr  
 35 40 45  
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu  
 50 55 60  
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp

65					70					75				80
Ile	Phe	Ala	Pro	Glu	Phe	Gln	Pro	Ile	Asp	Lys	Tyr	Ala	Val	Glu Asp
				85					90					95
Tyr	Arg	Gly	Ala	Val	Glu	Ala	Leu	Gln	Ile	Arg	Pro	Phe	Ala	Leu Val
			100					105					110	
Asn	Ala	Val	Ala	Ser	Gln	Met	Lys	Lys	Arg	Lys	Ser	Gly	His	Ile Ile
		115					120					125		
Phe	Ile	Thr	Ser	Ala	Thr	Pro	Phe	Gly	Pro	Trp	Lys	Glu	Leu	Ser Thr
	130					135					140			
Tyr	Thr	Ser	Ala	Arg	Ala	Gly	Ala	Cys	Thr	Leu	Ala	Asn	Ala	Leu Ser
145				150						155				160
Lys	Glu	Leu	Gly	Glu	Tyr	Asn	Ile	Pro	Val	Phe	Ala	Ile	Gly	Pro Asn
			165						170				175	
Tyr	Leu	His	Ser	Glu	Asp	Ser	Pro	Tyr	Phe	Tyr	Pro	Thr	Glu	Pro Trp
			180					185					190	
Lys	Thr	Asn	Pro	Glu	His	Val	Ala	His	Val	Lys	Lys	Val	Thr	Ala Leu
		195					200					205		
Gln	Arg	Leu	Gly	Thr	Gln	Lys	Glu	Leu	Gly	Glu	Leu	Val	Ala	Phe Leu
	210					215					220			
Ala	Ser	Gly	Ser	Cys	Asp	Tyr	Leu	Thr	Gly	Gln	Val	Phe	Trp	Leu Ala
225					230					235				240
Gly	Gly	Phe	Pro	Met	Ile	Glu	Arg	Trp	Pro	Gly	Met	Pro	Glu	
				245					250					

<210> 39  
 <211> 855  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> KRED krh133c

<221> CDS  
 <222> (1)...(852)

<400> 39	
atg gct aaa aac ttt agc aat gtc gaa tat cct gcc ccg ccg cca gct	48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala	
1 5 10 15	
cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac	96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn	
20 25 30	
ggc aaa gtc gcg tct atc acc ggt agc agc tca ggc att ggt tac gcg	144
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala	
35 40 45	
ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat	192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr	
50 55 60	
aac agc cag gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat	240
Asn Ser Gln Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr	
65 70 75 80	
ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg	288

Gly	Val	Lys	Val	Lys	Ala	Tyr	Lys	Ala	Asn	Val	Ser	Ser	Ser	Asp	Ala		
				85					90					95			
gtg	aaa	cag	act	att	gag	cag	cag	atc	aag	gat	ttt	ggc	cac	ctg	gac		336
Val	Lys	Gln	Thr	Ile	Glu	Gln	Gln	Ile	Lys	Asp	Phe	Gly	His	Leu	Asp		
			100					105					110				
att	gtt	gtg	gcg	aac	gca	ggc	atc	cca	tgg	act	aag	ggg	gca	tac	atc		384
Ile	Val	Val	Ala	Asn	Ala	Gly	Ile	Pro	Trp	Thr	Lys	Gly	Ala	Tyr	Ile		
			115				120						125				
gat	cag	gat	gac	gat	aaa	cat	ttt	gac	cag	gtg	gtg	gac	gtc	gac	ctg		432
Asp	Gln	Asp	Asp	Asp	Lys	His	Phe	Asp	Gln	Val	Val	Asp	Val	Asp	Leu		
			130			135							140				
aaa	ggc	gta	ggc	tat	gta	gca	aaa	cat	gcg	ggg	cgc	cat	tat	cgt	gaa		480
Lys	Gly	Val	Gly	Tyr	Val	Ala	Lys	His	Ala	Gly	Arg	His	Tyr	Arg	Glu		
					150					155					160		
cgt	ttc	gaa	aaa	gaa	ggc	aaa	aag	ggc	gcc	ttg	gtt	ttt	acg	gct	tcc		528
Arg	Phe	Glu	Lys	Glu	Gly	Lys	Lys	Gly	Ala	Leu	Val	Phe	Thr	Ala	Ser		
				165					170						175		
atg	tcg	ggg	cac	atc	gtt	aac	gtg	ccg	caa	ttt	cag	gcg	acc	tac	aat		576
Met	Ser	Gly	His	Ile	Val	Asn	Val	Pro	Gln	Phe	Gln	Ala	Thr	Tyr	Asn		
			180					185					190				
gcg	gcc	aag	gca	ggc	gtg	cgt	cat	ttc	gca	aag	tcc	ctg	gcc	gtg	gaa		624
Ala	Ala	Lys	Ala	Gly	Val	Arg	His	Phe	Ala	Lys	Ser	Leu	Ala	Val	Glu		
			195				200						205				
ttt	gct	cct	ttc	gca	cgt	gtt	aac	tct	gta	tct	cct	ggc	tat	att	aat		672
Phe	Ala	Pro	Phe	Ala	Arg	Val	Asn	Ser	Val	Ser	Pro	Gly	Tyr	Ile	Asn		
			210			215					220						
acc	gag	atc	tct	gat	ttc	gtc	ccg	caa	gaa	aca	caa	aat	aaa	tgg	tgg		720
Thr	Glu	Ile	Ser	Asp	Phe	Val	Pro	Gln	Glu	Thr	Gln	Asn	Lys	Trp	Trp		
					230				235						240		
agc	tta	gtt	cca	ttg	ggg	cgt	ggg	ggg	gaa	act	gcg	gaa	tta	gtt	ggg		768
Ser	Leu	Val	Pro	Leu	Gly	Arg	Gly	Gly	Glu	Thr	Ala	Glu	Leu	Val	Gly		
				245				250						255			
gcc	tac	ctg	ttc	ctg	gca	agt	gat	gcg	ggc	tcc	tac	gcc	acg	ggc	aca		816
Ala	Tyr	Leu	Phe	Leu	Ala	Ser	Asp	Ala	Gly	Ser	Tyr	Ala	Thr	Gly	Thr		
			260					265					270				
gat	atc	att	gtg	gat	ggc	ggc	tac	acg	ctg	ccg	taa	tga					855
Asp	Ile	Ile	Val	Asp	Gly	Gly	Tyr	Thr	Leu	Pro	*						
			275				280										

<210> 40

<211> 283

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED krh133c

<400> 40

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Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
1      5      10      15
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
20     25     30
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
35     40     45
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
50     55     60
Asn Ser Gln Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65     70     75     80
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
85     90     95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
100    105    110
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
115    120    125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
130    135    140
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Tyr Arg Glu
145    150    155    160
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
165    170    175
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
180    185    190
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
195    200    205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
210    215    220
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225    230    235    240
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
245    250    255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
260    265    270
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
275    280
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<210> 41

<211> 855

<212> DNA

<213> Artificial Sequence

<220>

<223> KRED krh215

<221> CDS

<222> (1)...(855)

<400> 41

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atg gct aaa aac ttt agc aat gtc gaa tat cct gcc ccg ccg cca gct
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
1      5      10      15
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48



cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn 20 25 30	96
ggc aaa gtc gcg tct atc acc ggt agc agc tca ggc att ggt tac gcg Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala 35 40 45	144
ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr 50 55 60	192
aac agc cag gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat Asn Ser Gln Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr 65 70 75 80	240
ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala 85 90 95	288
gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp 100 105 110	336
att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile 115 120 125	384
gat cag gat gac gat aaa cat ttt gac cag gtg att gac gtc gac ctg Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Ile Asp Val Asp Leu 130 135 140	432
aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat tat cgt gaa Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Tyr Arg Glu 145 150 155 160	480
cgt ttc gaa aaa gaa ggc ata aag ggc gcc ttg att ttt acg gct tcc Arg Phe Glu Lys Glu Gly Ile Lys Gly Ala Leu Ile Phe Thr Ala Ser 165 170 175	528
gtg tcg ggt cac atc gtt aac att ccg caa ttt cag gcg acc tac aat Val Ser Gly His Ile Val Asn Ile Pro Gln Phe Gln Ala Thr Tyr Asn 180 185 190	576
gcg gcc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu 195 200 205	624
ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn 210 215 220	672
acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp 225 230 235 240	720
agc tta gtt cca ttg ggt cgt ggt ggg gaa act gcg gaa tta gtt ggt	768

Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly  
 245 250 255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca 816  
 Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr  
 260 265 270

gat atc att gtg gat ggc ggc tac acg ctg ccg taa tga 855  
 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro \* \*  
 275 280

<210> 42  
 <211> 283  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> KRED krh215

<400> 42  
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 1 5 10 15  
 His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn  
 20 25 30  
 Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala  
 35 40 45  
 Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr  
 50 55 60  
 Asn Ser Gln Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr  
 65 70 75 80  
 Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala  
 85 90 95  
 Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp  
 100 105 110  
 Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile  
 115 120 125  
 Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Ile Asp Val Asp Leu  
 130 135 140  
 Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Tyr Arg Glu  
 145 150 155 160  
 Arg Phe Glu Lys Glu Gly Ile Lys Gly Ala Leu Ile Phe Thr Ala Ser  
 165 170 175  
 Val Ser Gly His Ile Val Asn Ile Pro Gln Phe Gln Ala Thr Tyr Asn  
 180 185 190  
 Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu  
 195 200 205  
 Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn  
 210 215 220  
 Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp  
 225 230 235 240  
 Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly  
 245 250 255  
 Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr  
 260 265 270  
 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  
 275 280

<210> 43  
 <211> 855  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> KRED krh267

<221> CDS  
 <222> (1)...(855)

<400> 43  
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 Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala  
 1 5 10 15  
 cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac 96  
 His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn  
 20 25 30  
 ggc aaa gtc gcg tct atc acc ggt agc agc tca ggc att ggt tac gcg 144  
 Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala  
 35 40 45  
 ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat 192  
 Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr  
 50 55 60  
 aac agc cag gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat 240  
 Asn Ser Gln Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr  
 65 70 75 80  
 ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg 288  
 Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala  
 85 90 95  
 gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac 336  
 Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp  
 100 105 110  
 att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc 384  
 Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile  
 115 120 125  
 gat cag gat gac gat aag cat ttt gac cag gtg att gac gtc gac ctg 432  
 Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Ile Asp Val Asp Leu  
 130 135 140  
 aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ctt cgt gaa 480  
 Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Leu Arg Glu  
 145 150 155 160  
 cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc 528  
 Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser  
 165 170 175

acg tcg ggt cac atc gtt aac att ccg caa ttt cag gcg acc tac aat 576  
 Thr Ser Gly His Ile Val Asn Ile Pro Gln Phe Gln Ala Thr Tyr Asn  
 180 185 190

gcg gcc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa 624  
 Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu  
 195 200 205

ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat 672  
 Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn  
 210 215 220

acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg 720  
 Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp  
 225 230 235 240

agc tta gtt cca ttg ggt cgt ggt ggg gaa act gcg gaa tta gtt ggt 768  
 Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly  
 245 250 255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca 816  
 Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr  
 260 265 270

gat atc att gtg gat ggc ggc tac acg ctg ccg taa tga 855  
 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro \* \*  
 275 280

<210> 44  
 <211> 283  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> KRED krh267

<400> 44  
 Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala  
 1 5 10 15  
 His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn  
 20 25 30  
 Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala  
 35 40 45  
 Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr  
 50 55 60  
 Asn Ser Gln Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr  
 65 70 75 80  
 Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala  
 85 90 95  
 Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp  
 100 105 110  
 Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile  
 115 120 125  
 Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Ile Asp Val Asp Leu  
 130 135 140  
 Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Leu Arg Glu

145		150		155		160
Arg Phe Glu Lys	Glu Gly Lys Lys Gly Ala	Leu Val Phe Thr Ala Ser				
	165	170		175		
Thr Ser Gly His	Ile Val Asn Ile Pro Gln Phe Gln Ala Thr Tyr Asn					
	180	185		190		
Ala Ala Lys Ala	Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu					
	195	200		205		
Phe Ala Pro Phe	Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn					
	210	215		220		
Thr Glu Ile Ser	Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp					
225	230	235		240		
Ser Leu Val Pro	Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly					
	245	250		255		
Ala Tyr Leu Phe	Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr					
	260	265		270		
Asp Ile Ile Val	Asp Gly Gly Tyr Thr Leu Pro					
	275	280				

<210> 45  
 <211> 855  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> KRED krh287

<221> CDS  
 <222> (1)...(855)

<400> 45	
atg gct aaa aac ttt agc aat gtc gaa tac cct gcc ccg ccg cca gct	48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala	
1 5 10 15	
cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac	96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn	
20 25 30	
ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg	144
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala	
35 40 45	
ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat	192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr	
50 55 60	
aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat	240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr	
65 70 75 80	
ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg	288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala	
85 90 95	
gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac	336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp	
100 105 110	

att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile 115 120 125	384
gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu 130 135 140	432
aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu 145 150 155 160	480
cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser 165 170 175	528
atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg acc tac aat Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn 180 185 190	576
gcg gcc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu 195 200 205	624
ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn 210 215 220	672
acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp 225 230 235 240	720
agc tta gtt cca ttg ggc cgt ggt ggg gaa act gcg gaa tta gtt ggt Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly 245 250 255	768
gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr 260 265 270	816
gat atc att gtg gac ggc ggc tac acg ctg ccg taa tga Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro * * 275 280	855

<210> 46  
 <211> 283  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> KRED\_krh287

<400> 46  
 Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala  
 1 5 10 15

His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn  
                   20                  25                  30  
 Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala  
                   35                  40                  45  
 Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr  
                   50                  55                  60  
 Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr  
                   65                  70                  75                  80  
 Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala  
                   85                  90                  95  
 Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp  
                   100                  105                  110  
 Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile  
                   115                  120                  125  
 Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu  
                   130                  135                  140  
 Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu  
                   145                  150                  155                  160  
 Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser  
                   165                  170                  175  
 Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn  
                   180                  185                  190  
 Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu  
                   195                  200                  205  
 Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn  
                   210                  215                  220  
 Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp  
                   225                  230                  235                  240  
 Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly  
                   245                  250                  255  
 Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr  
                   260                  265                  270  
 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  
                   275                  280

<210> 47

<211> 855

<212> DNA

<213> Artificial Sequence

<220>

<223> KRED krh320

<221> CDS

<222> (1)...(855)

<400> 47

atg gct aaa aac ttt agc aat gtc gaa tac cct gcc ccg ccg cca gct  
 Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala  
   1                  5                  10                  15

48

cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac  
 His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn  
                   20                  25                  30

96

ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg  
 Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala

144

35	40	45	
ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr 50 55 60			192
aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr 65 70 75 80			240
ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt tat gcg Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Tyr Ala 85 90 95			288
gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp 100 105 110			336
att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile 115 120 125			384
gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu 130 135 140			432
aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu 145 150 155 160			480
cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser 165 170 175			528
atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg acc tac aat Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn 180 185 190			576
gcg gcc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu 195 200 205			624
ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn 210 215 220			672
acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp 225 230 235 240			720
agc tta gtt cca ttg ggc cgt ggt ggg gaa act gcg gaa tta gtt ggt Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly 245 250 255			768
gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr 260 265 270			816



gat atc att gtg gac ggc ggc tac acg ctg ccg taa tga  
 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro \* \*  
           275                                  280

855

<210> 48  
 <211> 283  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> KRED krh320

<400> 48  
 Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala  
   1                          5                          10                          15  
 His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn  
           20                          25                          30  
 Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala  
           35                          40                          45  
 Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr  
           50                          55                          60  
 Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr  
   65                          70                          75                          80  
 Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Tyr Ala  
           85                          90                          95  
 Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp  
           100                          105                          110  
 Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile  
           115                          120                          125  
 Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu  
   130                          135                          140  
 Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu  
   145                          150                          155                          160  
 Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser  
           165                          170                          175  
 Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn  
           180                          185                          190  
 Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu  
           195                          200                          205  
 Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn  
   210                          215                          220  
 Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp  
   225                          230                          235                          240  
 Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly  
           245                          250                          255  
 Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr  
           260                          265                          270  
 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  
           275                          280

<210> 49  
 <211> 852  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> KRED krh326

<221> CDS

<222> (1)... (852)

<400> 49

atg gct aaa aac ttt agc aat gtc gaa tac cct gcc ccg ccg cca gct	48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala	
1 5 10 15	

cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac	96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn	
20 25 30	

ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg	144
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala	
35 40 45	

ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat	192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr	
50 55 60	

aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat	240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr	
65 70 75 80	

ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg	288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala	
85 90 95	

gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac	336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp	
100 105 110	

att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc	384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile	
115 120 125	

gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg	432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu	
130 135 140	

aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa	480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu	
145 150 155 160	

cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc	528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser	
165 170 175	

atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg acc tac aat	576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn	
180 185 190	

gcg gtc aag gca ggc gtg cgt cac ttc gca aag tcc ctg gcc gtg gaa	624
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu	

195	200	205	
ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat			672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn			
210	215	220	
acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg			720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp			
225	230	235	240
agc tta gtt cca ttg ggt cgt ggt ggg gaa act gcg gaa tta gtt ggt			768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly			
	245	250	255
gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca			816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr			
	260	265	270
gat atc att gtg gac ggc ggc tac acg ctg ccg taa			852
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro *			
275	280		

<210> 50  
 <211> 283  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> KRED krh326

<400> 50

Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala			
1	5	10	15
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn			
	20	25	30
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala			
	35	40	45
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr			
	50	55	60
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr			
65	70	75	80
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala			
	85	90	95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp			
	100	105	110
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile			
	115	120	125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu			
	130	135	140
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu			
145	150	155	160
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser			
	165	170	175
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn			
	180	185	190
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu			

	195		200		205										
Phe	Ala	Pro	Phe	Ala	Arg	Val	Asn	Ser	Val	Ser	Pro	Gly	Tyr	Ile	Asn
	210					215					220				
Thr	Glu	Ile	Ser	Asp	Phe	Val	Pro	Gln	Glu	Thr	Gln	Asn	Lys	Trp	Trp
225					230					235					240
Ser	Leu	Val	Pro	Leu	Gly	Arg	Gly	Gly	Glu	Thr	Ala	Glu	Leu	Val	Gly
				245					250					255	
Ala	Tyr	Leu	Phe	Leu	Ala	Ser	Asp	Ala	Gly	Ser	Tyr	Ala	Thr	Gly	Thr
		260					265					270			
Asp	Ile	Ile	Val	Asp	Gly	Gly	Tyr	Thr	Leu	Pro					
	275					280									

<210> 51  
 <211> 852  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> KRED krh408

<221> CDS  
 <222> (1)...(852)

<400> 51	
atg gct aaa aac ttt agc aat gtc gaa tac cct gcc ccg ccg cca gct	48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala	
1 5 10 15	
cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac	96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn	
20 25 30	
ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg	144
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala	
35 40 45	
ctg gcc gaa gct ttt gcg cag gct ggc gca gac gtt gcg atc tgg tat	192
Leu Ala Glu Ala Phe Ala Gln Ala Gly Ala Asp Val Ala Ile Trp Tyr	
50 55 60	
aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat	240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr	
65 70 75 80	
ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg	288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala	
85 90 95	
gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac	336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp	
100 105 110	
att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc	384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile	
115 120 125	
gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg	432

Asp	Gln	Asp	Asp	Asp	Lys	His	Phe	Asp	Gln	Val	Val	Asp	Val	Asp	Leu	
130						135					140					
aaa	ggc	gta	ggc	tat	gta	gca	aaa	cat	gcg	ggt	cgc	cat	ttt	cgt	gaa	480
Lys	Gly	Val	Gly	Tyr	Val	Ala	Lys	His	Ala	Gly	Arg	His	Phe	Arg	Glu	
145					150				155					160		
cgt	tcc	gaa	aaa	gaa	ggc	aaa	aag	ggc	gcc	ttg	gtt	ttt	acg	gct	tcc	528
Arg	Ser	Glu	Lys	Glu	Gly	Lys	Lys	Gly	Ala	Leu	Val	Phe	Thr	Ala	Ser	
				165				170					175			
atg	tcg	ggg	cac	atc	gtt	aac	gtg	ccg	caa	ttt	cag	gcg	acc	tac	aac	576
Met	Ser	Gly	His	Ile	Val	Asn	Val	Pro	Gln	Phe	Gln	Ala	Thr	Tyr	Asn	
			180					185					190			
gcg	gtc	aag	gca	ggc	gtg	cgt	cat	ttc	gca	aag	tcc	ctg	gcc	gtg	gaa	624
Ala	Val	Lys	Ala	Gly	Val	Arg	His	Phe	Ala	Lys	Ser	Leu	Ala	Val	Glu	
		195					200					205				
ttt	gct	cct	ttc	gca	cgt	gtt	aac	tct	gta	tct	cct	ggc	tat	att	aat	672
Phe	Ala	Pro	Phe	Ala	Arg	Val	Asn	Ser	Val	Ser	Pro	Gly	Tyr	Ile	Asn	
	210					215					220					
acc	gag	atc	tct	gat	ttc	gtc	ccg	caa	gaa	aca	caa	aat	aaa	tgg	tgg	720
Thr	Glu	Ile	Ser	Asp	Phe	Val	Pro	Gln	Glu	Thr	Gln	Asn	Lys	Trp	Trp	
225					230				235					240		
agc	tta	gtt	cca	ttg	ggg	cgt	ggg	ggg	gaa	act	gcg	gaa	tta	gtt	ggg	768
Ser	Leu	Val	Pro	Leu	Gly	Arg	Gly	Gly	Glu	Thr	Ala	Glu	Leu	Val	Gly	
				245				250					255			
gcc	tac	ctg	ttc	ctg	gca	agt	gat	gcg	ggc	tcc	tac	gcc	acg	ggc	aca	816
Ala	Tyr	Leu	Phe	Leu	Ala	Ser	Asp	Ala	Gly	Ser	Tyr	Ala	Thr	Gly	Thr	
			260					265					270			
gat	atc	att	gtg	gac	ggc	ggc	tac	acg	ctg	ccg	taa					852
Asp	Ile	Ile	Val	Asp	Gly	Gly	Tyr	Thr	Leu	Pro	*					
	275						280									

<210> 52

<211> 283

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED krh408

<400> 52

Met	Ala	Lys	Asn	Phe	Ser	Asn	Val	Glu	Tyr	Pro	Ala	Pro	Pro	Pro	Ala	
1				5				10						15		
His	Thr	Lys	Asn	Glu	Ser	Leu	Gln	Val	Leu	Asp	Leu	Phe	Lys	Leu	Asn	
			20					25					30			
Gly	Lys	Val	Ala	Ser	Ile	Thr	Gly	Ser	Asn	Ser	Gly	Ile	Gly	Tyr	Ala	
		35					40					45				
Leu	Ala	Glu	Ala	Phe	Ala	Gln	Ala	Gly	Ala	Asp	Val	Ala	Ile	Trp	Tyr	
	50					55					60					

Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr  
 65 70 75 80  
 Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala  
 85 90 95  
 Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp  
 100 105 110  
 Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile  
 115 120 125  
 Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu  
 130 135 140  
 Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu  
 145 150 155 160  
 Arg Ser Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser  
 165 170 175  
 Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn  
 180 185 190  
 Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu  
 195 200 205  
 Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn  
 210 215 220  
 Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp  
 225 230 235 240  
 Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly  
 245 250 255  
 Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr  
 260 265 270  
 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  
 275 280

<210> 53  
 <211> 852  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> KRED krh417

<221> CDS  
 <222> (1)...(852)

<400> 53  
 atg gct aaa aac ttt agc aat gtc gaa tat cct gcc ccg ccg cca gct 48  
 Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala  
 1 5 10 15  
 cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac 96  
 His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn  
 20 25 30  
 ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg 144  
 Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala  
 35 40 45  
 ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat 192  
 Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr  
 50 55 60

aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat	240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr	
65 70 75 80	
ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg	288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala	
85 90 95	
gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac	336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp	
100 105 110	
att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc	384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile	
115 120 125	
gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg	432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu	
130 135 140	
aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa	480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu	
145 150 155 160	
cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc	528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser	
165 170 175	
atg tcg ggt cac atc gtt aac att ccg caa ttt cag gcg acc tac aat	576
Met Ser Gly His Ile Val Asn Ile Pro Gln Phe Gln Ala Thr Tyr Asn	
180 185 190	
gcg gcc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa	624
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu	
195 200 205	
ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat	672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn	
210 215 220	
acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg	720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp	
225 230 235 240	
agc tta gtc cca ttg ggt cgt ggt ggg gaa act gcg gaa tta gtt ggt	768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly	
245 250 255	
gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca	816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr	
260 265 270	
gat atc att gtg gat ggc ggc tac acg ctg ccg taa	852
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro *	
275 280	

<210> 54  
 <211> 283  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> KRED krh417

<400> 54  
 Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Ala  
 1 5 10 15  
 His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn  
 20 25 30  
 Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala  
 35 40 45  
 Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr  
 50 55 60  
 Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr  
 65 70 75 80  
 Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala  
 85 90 95  
 Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp  
 100 105 110  
 Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile  
 115 120 125  
 Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu  
 130 135 140  
 Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu  
 145 150 155 160  
 Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser  
 165 170 175  
 Met Ser Gly His Ile Val Asn Ile Pro Gln Phe Gln Ala Thr Tyr Asn  
 180 185 190  
 Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu  
 195 200 205  
 Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn  
 210 215 220  
 Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp  
 225 230 235 240  
 Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly  
 245 250 255  
 Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr  
 260 265 270  
 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  
 275 280

<210> 55  
 <211> 852  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> KRED krh483

<221> CDS  
 <222> (1)...(852)



<400> 55

atg gct aaa aac ttt tcc aat gtc gaa tat cct gcc ccg ccg cca gct	48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala	
1 5 10 15	
cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac	96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn	
20 25 30	
ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg	144
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala	
35 40 45	
ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat	192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr	
50 55 60	
aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat	240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr	
65 70 75 80	
ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg	288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala	
85 90 95	
gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac	336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp	
100 105 110	
ata gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc	384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile	
115 120 125	
gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg	432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu	
130 135 140	
aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa	480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu	
145 150 155 160	
cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc	528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser	
165 170 175	
atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg acc tac aat	576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn	
180 185 190	
gcg gtc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa	624
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu	
195 200 205	
ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat	672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn	
210 215 220	

acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg 720  
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp  
225 230 235 240

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca 816  
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr  
260 265 270

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<210> 56
<211> 283
<212> PRT
<213> Artificial Sequence
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<400> 56															
Met	Ala	Lys	Asn	Phe	Ser	Asn	Val	Glu	Tyr	Pro	Ala	Pro	Pro	Pro	Ala
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			20					25					30		
Gly	Lys	Val	Ala	Ser	Ile	Thr	Gly	Ser	Asn	Ser	Gly	Ile	Gly	Tyr	Ala
		35					40					45			
Leu	Ala	Glu	Ala	Phe	Ala	Gln	Val	Gly	Ala	Asp	Val	Ala	Ile	Trp	Tyr
	50					55				60					
Asn	Ser	His	Asp	Ala	Thr	Gly	Lys	Ala	Glu	Ala	Leu	Ala	Lys	Lys	Tyr
65					70					75				80	
Gly	Val	Lys	Val	Lys	Ala	Tyr	Lys	Ala	Asn	Val	Ser	Ser	Ser	Asp	Ala
				85					90					95	
Val	Lys	Gln	Thr	Ile	Glu	Gln	Gln	Ile	Lys	Asp	Phe	Gly	His	Leu	Asp
			100					105					110		
Ile	Val	Val	Ala	Asn	Ala	Gly	Ile	Pro	Trp	Thr	Lys	Gly	Ala	Tyr	Ile
		115				120						125			
Asp	Gln	Asp	Asp	Asp	Lys	His	Phe	Asp	Gln	Val	Val	Asp	Val	Asp	Leu
	130					135					140				
Lys	Gly	Val	Gly	Tyr	Val	Ala	Lys	His	Ala	Gly	Arg	His	Phe	Arg	Glu
145					150					155					160
Arg	Phe	Glu	Lys	Glu	Gly	Lys	Lys	Gly	Ala	Leu	Val	Phe	Thr	Ala	Ser
				165					170					175	
Met	Ser	Gly	His	Ile	Val	Asn	Val	Pro	Gln	Phe	Gln	Ala	Thr	Tyr	Asn
			180					185					190		
Ala	Val	Lys	Ala	Gly	Val	Arg	His	Phe	Ala	Lys	Ser	Leu	Ala	Val	Glu
		195				200					205				
Phe	Ala	Pro	Phe	Ala	Arg	Val	Asn	Ser	Val	Ser	Pro	Gly	Tyr	Ile	Asn
	210					215					220				
Thr	Glu	Ile	Ser	Asp	Phe	Val	Pro	Gln	Glu	Thr	Gln	Asn	Lys	Trp	Trp
225				230						235					240
Ser	Leu	Val	Pro	Leu	Gly	Arg	Gly	Gly	Glu	Thr	Ala	Glu	Leu	Val	Gly

				245						250					255				
Ala	Tyr	Leu	Phe	Leu	Ala	Ser	Asp	Ala	Gly	Ser	Tyr	Ala	Thr	Gly	Thr				
			260					265						270					
Asp	Ile	Ile	Val	Asp	Gly	Gly	Tyr	Thr	Leu	Pro									
		275					280												

<210> 57  
 <211> 852  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> KRED krh476

<221> CDS  
 <222> (1)...(852)

<400> 57																			
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Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala																			
1 5 10 15																			
cat acc aaa gac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac																			96
His Thr Lys Asp Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn																			
20 25 30																			
ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg																			144
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala																			
35 40 45																			
ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat																			192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr																			
50 55 60																			
aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat																			240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr																			
65 70 75 80																			
ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg																			288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala																			
85 90 95																			
gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac																			336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp																			
100 105 110																			
att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc																			384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile																			
115 120 125																			
gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg																			432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu																			
130 135 140																			
aaa ggc gta ggc tat gta gcg aaa cat gcg ggt cgc cat ttt cgt gaa																			480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu																			
145 150 155 160																			

cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc	528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser	
165 170 175	
atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg acc tac aat	576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn	
180 185 190	
gcg gtc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa	624
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu	
195 200 205	
ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat	672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn	
210 215 220	
acc gag atc tct gat ttc gtc ccg caa gaa aca cag aat aaa tgg tgg	720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp	
225 230 235 240	
agc tta gtt cca ttg ggc cgt ggt ggg gaa act gcg gaa tta gtt ggt	768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly	
245 250 255	
gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca	816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr	
260 265 270	
gat atc att gtg gac ggc ggc tac acg ctg ccg taa	852
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro *	
275 280	

<210> 58  
 <211> 283  
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 <213> Artificial Sequence

<220>  
 <223> KRED krh476

<400> 58

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His Thr Lys Asp Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn	
20 25 30	
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala	
35 40 45	
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr	
50 55 60	
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr	
65 70 75 80	
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala	
85 90 95	
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp	
100 105 110	

Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile  
 115 120 125  
 Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu  
 130 135 140  
 Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu  
 145 150 155 160  
 Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser  
 165 170 175  
 Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn  
 180 185 190  
 Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu  
 195 200 205  
 Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn  
 210 215 220  
 Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp  
 225 230 235 240  
 Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly  
 245 250 255  
 Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr  
 260 265 270  
 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  
 275 280

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<221> CDS  
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 cat acc aaa gac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac 96  
 His Thr Lys Asp Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn  
 20 25 30  
 ggc aaa gtc gcg tct atc acc ggt agc agc tca ggc att ggt tac gcg 144  
 Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala  
 35 40 45  
 ctg gcc gaa gcc ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat 192  
 Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr  
 50 55 60  
 aac agc cag gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat 240  
 Asn Ser Gln Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr  
 65 70 75 80  
 ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg 288  
 Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala

85										90					95					
gtg	aaa	cag	act	att	gag	cag	cag	atc	aag	gat	ttt	ggc	cac	ctg	gac	336				
Val	Lys	Gln	Thr	Ile	Glu	Gln	Gln	Ile	Lys	Asp	Phe	Gly	His	Leu	Asp					
100					105					110										
att	gtt	gtg	gcg	aac	gca	ggc	atc	cca	tgg	act	aag	ggg	gca	tac	atc	384				
Ile	Val	Val	Ala	Asn	Ala	Gly	Ile	Pro	Trp	Thr	Lys	Gly	Ala	Tyr	Ile					
115					120					125										
gat	cag	gat	gac	gat	aaa	cat	ttt	gac	cag	gtg	att	gac	gtc	gac	ctg	432				
Asp	Gln	Asp	Asp	Asp	Lys	His	Phe	Asp	Gln	Val	Ile	Asp	Val	Asp	Leu					
130					135					140										
aaa	ggc	gta	ggc	tat	gta	gca	aaa	cat	gcg	ggg	cgc	cat	tat	cgt	gaa	480				
Lys	Gly	Val	Gly	Tyr	Val	Ala	Lys	His	Ala	Gly	Arg	His	Tyr	Arg	Glu					
145					150					155					160					
cgt	ttc	gaa	aaa	gaa	ggc	ata	aag	ggc	gcc	ttg	att	ttt	acg	gct	tcc	528				
Arg	Phe	Glu	Lys	Glu	Gly	Ile	Lys	Gly	Ala	Leu	Ile	Phe	Thr	Ala	Ser					
165					170					175										
gtg	tcg	ggg	cac	atc	gtt	aac	att	ccg	caa	ttt	cag	gcg	acc	tac	aat	576				
Val	Ser	Gly	His	Ile	Val	Asn	Ile	Pro	Gln	Phe	Gln	Ala	Thr	Tyr	Asn					
180					185					190										
gcg	gcc	aag	gca	ggc	gtg	cgt	cat	ttc	gca	aag	tcc	ctg	gcc	gtg	gaa	624				
Ala	Ala	Lys	Ala	Gly	Val	Arg	His	Phe	Ala	Lys	Ser	Leu	Ala	Val	Glu					
195					200					205										
ttt	gct	cct	ttc	gca	cgt	gtt	aac	tct	gta	tct	cct	ggc	tat	att	aat	672				
Phe	Ala	Pro	Phe	Ala	Arg	Val	Asn	Ser	Val	Ser	Pro	Gly	Tyr	Ile	Asn					
210					215					220										
acc	gag	atc	tct	gat	ttc	gtc	ccg	caa	gaa	aca	caa	aat	aaa	tgg	tgg	720				
Thr	Glu	Ile	Ser	Asp	Phe	Val	Pro	Gln	Glu	Thr	Gln	Asn	Lys	Trp	Trp					
225					230					235					240					
agc	tta	gtt	cca	ttg	ggg	cgt	ggg	ggg	gaa	act	gcg	gaa	tta	gtt	ggg	768				
Ser	Leu	Val	Pro	Leu	Gly	Arg	Gly	Gly	Glu	Thr	Ala	Glu	Leu	Val	Gly					
245					250					255										
gcc	tac	ctg	ttc	ctg	gca	agt	gat	gcg	ggc	tcc	tac	gcc	acg	ggc	aca	816				
Ala	Tyr	Leu	Phe	Leu	Ala	Ser	Asp	Ala	Gly	Ser	Tyr	Ala	Thr	Gly	Thr					
260					265					270										
gat	atc	att	gtg	gat	ggc	ggc	tac	acg	ctg	ccg	taa					852				
Asp	Ile	Ile	Val	Asp	Gly	Gly	Tyr	Thr	Leu	Pro	*									
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<210> 60  
 <211> 283  
 <212> PRT  
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<223> KRED krh495

<400> 60

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His Thr Lys Asp Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
 20          25          30
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
 35          40          45
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
 50          55          60
Asn Ser Gln Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
 65          70          75          80
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
 85          90          95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
100          105          110
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
115          120          125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Ile Asp Val Asp Leu
130          135          140
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Tyr Arg Glu
145          150          155          160
Arg Phe Glu Lys Glu Gly Ile Lys Gly Ala Leu Ile Phe Thr Ala Ser
165          170          175
Val Ser Gly His Ile Val Asn Ile Pro Gln Phe Gln Ala Thr Tyr Asn
180          185          190
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
195          200          205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
210          215          220
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225          230          235          240
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
245          250          255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
260          265          270
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
275          280
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<210> 61

<211> 789

<212> DNA

<213> Artificial Sequence

<220>

<223> GDH 2313

<221> CDS

<222> (1)...(789)

<400> 61

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 1          5          10          15

tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag gag cag gca      96
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Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala	
20 25 30	
aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg aac gag gta	144
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val	
35 40 45	
aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc gtc caa gga	192
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly	
50 55 60	
gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa acg gca att	240
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile	
65 70 75 80	
aag gag ttc ggc aca ctc gat att atg att aat aat gcc ggt ctt gaa	288
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu	
85 90 95	
aat cct gtg cca tct cac gaa atg ccg ctc aag gat tgg gat aaa gtc	336
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val	
100 105 110	
atc ggc acg aac tta acg ggt gcc ttt tta gga agc cgt gaa gcg att	384
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile	
115 120 125	
aaa tat ttc gta gaa aac gat atc aag gga aat gtc att aac atg tcc	432
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser	
130 135 140	
agt gtg cac gaa gtg att cct tgg ccg tta ttt gtc cac tat gcg gca	480
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala	
145 150 155 160	
agt aaa ggc ggg atg aag ctg atg aca gaa aca tta gcg ttg gaa tac	528
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr	
165 170 175	
gcg ccg aag ggc att cgc gtc aat aat att ggg cca ggt gcg atc aac	576
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn	
180 185 190	
acg acg atc aat gct gag aaa ttt gct gac cct aaa cag aaa gct gat	624
Thr Thr Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp	
195 200 205	
gta gaa agc atg att cca atg gga tat atc ggc gaa ccg gag gag atc	672
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile	
210 215 220	
gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc agc tac gtc aca	720
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr	
225 230 235 240	
ggc atc acg tta ttc gcg gac ggc ggt atg aca caa tat cct tca ttc	768
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe	



245  
 cag gca ggc cgc ggt taa tga  
 Gln Ala Gly Arg Gly \* \*  
 260

250

255

789

<210> 62  
 <211> 261  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> GDH 2313

<400> 62  
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 Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala  
 20 25 30  
 Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val  
 35 40 45  
 Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Gln Gly  
 50 55 60  
 Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile  
 65 70 75 80  
 Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu  
 85 90 95  
 Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val  
 100 105 110  
 Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile  
 115 120 125  
 Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser  
 130 135 140  
 Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala  
 145 150 155 160  
 Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr  
 165 170 175  
 Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn  
 180 185 190  
 Thr Thr Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp  
 195 200 205  
 Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile  
 210 215 220  
 Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr  
 225 230 235 240  
 Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe  
 245 250 255  
 Gln Ala Gly Arg Gly  
 260

<210> 63  
 <211> 789  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> GDH 2331

<221> CDS

<222> (1) ... (789)

<400> 63

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1				5				10					15			

tca	ggg	ctc	gga	aag	gcg	atg	gcc	att	cgc	ttc	ggc	aag	gag	cag	gca	96
Ser	Gly	Leu	Gly	Lys	Ala	Met	Ala	Ile	Arg	Phe	Gly	Lys	Glu	Gln	Ala	
			20				25						30			

aaa	gtg	gtt	atc	aac	tat	tat	agt	aat	aaa	caa	gat	ccg	aac	gag	gta	144
Lys	Val	Val	Ile	Asn	Tyr	Tyr	Ser	Asn	Lys	Gln	Asp	Pro	Asn	Glu	Val	
			35				40					45				

aaa	gaa	gag	gtc	atc	aag	gcg	ggc	ggg	gaa	gct	gtt	gtc	gtc	caa	gga	192
Lys	Glu	Glu	Val	Ile	Lys	Ala	Gly	Gly	Glu	Ala	Val	Val	Val	Gln	Gly	
	50					55					60					

gat	gtc	acg	aaa	gag	gaa	gat	gta	aaa	aat	atc	gtg	caa	acg	gca	att	240
Asp	Val	Thr	Lys	Glu	Glu	Asp	Val	Lys	Asn	Ile	Val	Gln	Thr	Ala	Ile	
	65				70					75					80	

aag	gag	ttc	ggc	aca	ctc	gat	att	atg	att	aat	aat	gcc	ggg	ctt	gaa	288
Lys	Glu	Phe	Gly	Thr	Leu	Asp	Ile	Met	Ile	Asn	Asn	Ala	Gly	Leu	Glu	
				85					90					95		

aat	cct	gtg	cca	tct	cac	gaa	atg	ccg	ctc	aag	gat	tgg	gat	aaa	gtc	336
Asn	Pro	Val	Pro	Ser	His	Glu	Met	Pro	Leu	Lys	Asp	Trp	Asp	Lys	Val	
			100					105					110			

atc	ggc	acg	aac	tta	acg	ggg	gcc	ttt	tta	gga	agc	cgt	gaa	gcg	att	384
Ile	Gly	Thr	Asn	Leu	Thr	Gly	Ala	Phe	Leu	Gly	Ser	Arg	Glu	Ala	Ile	
			115				120					125				

aaa	tat	ttc	gta	gaa	aac	gat	atc	aag	gga	aat	gtc	att	aac	atg	tcc	432
Lys	Tyr	Phe	Val	Glu	Asn	Asp	Ile	Lys	Gly	Asn	Val	Ile	Asn	Met	Ser	
			130			135					140					

agt	gtg	cac	gaa	gtg	att	cct	tgg	ccg	tta	ttt	gtc	cac	tat	gcg	gca	480
Ser	Val	His	Glu	Val	Ile	Pro	Trp	Pro	Leu	Phe	Val	His	Tyr	Ala	Ala	
	145				150					155					160	

agt	aaa	ggc	ggg	atg	aag	ctg	atg	aca	gaa	aca	tta	gcg	ttg	gaa	tac	528
Ser	Lys	Gly	Gly	Met	Lys	Leu	Met	Thr	Glu	Thr	Leu	Ala	Leu	Glu	Tyr	
				165					170					175		

gcg	ccg	aag	ggc	att	cgc	gtc	aat	aat	att	ggg	cca	ggg	gcg	atc	aac	576
Ala	Pro	Lys	Gly	Ile	Arg	Val	Asn	Asn	Ile	Gly	Pro	Gly	Ala	Ile	Asn	
			180					185					190			

acg	cca	atc	aat	gct	gaa	aaa	ttc	gct	gac	cct	aaa	cag	aaa	gct	gat	624
Thr	Pro	Ile	Asn	Ala	Glu	Lys	Phe	Ala	Asp	Pro	Lys	Gln	Lys	Ala	Asp	
			195				200					205				

gcc gaa agc atg att cca atg gga tat atc ggc gaa ccg gag gag atc	672
Ala Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile	
210 215 220	
gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc agc tac gtc aca	720
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr	
225 230 235 240	
ggc gtc acg tta ttc gcg gac ggc ggt atg aca cta tat cct tca ttc	768
Gly Val Thr Leu Phe Ala Asp Gly Gly Met Thr Leu Tyr Pro Ser Phe	
245 250 255	
cag gca ggc cgc ggt taa tga	789
Gln Ala Gly Arg Gly * *	
260	

<210> 64  
 <211> 261  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> GDH 2331

<400> 64

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20 25 30	
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val	
35 40 45	
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly	
50 55 60	
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile	
65 70 75 80	
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu	
85 90 95	
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val	
100 105 110	
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile	
115 120 125	
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser	
130 135 140	
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala	
145 150 155 160	
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr	
165 170 175	
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn	
180 185 190	
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp	
195 200 205	
Ala Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile	
210 215 220	
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr	
225 230 235 240	



agt aaa ggc ggg atg aag ctg atg aca gaa aca tta gcg ttg gaa tac 528  
 Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr  
 165 170 175  
 gcg ccg aag ggc att cgc gtc aat aat att ggg cca ggt gcg atc aac 576  
 Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn  
 180 185 190  
 acg cca atc aat gct gaa aaa ttc gct gac cct aaa cag aaa gct gat 624  
 Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp  
 195 200 205  
 gcc gaa agc atg att cca atg gga tat atc ggc gaa ccg gag gag atc 672  
 Ala Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile  
 210 215 220  
 gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc agc tac gtc aca 720  
 Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr  
 225 230 235 240  
 ggc gtc acg tta ttc gcg gac ggc ggt atg aca caa tat cct tca ttc 768  
 Gly Val Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe  
 245 250 255  
 cag gca ggc cgc ggt taa tga 789  
 Gln Ala Gly Arg Gly \* \*  
 260

<210> 66  
 <211> 261  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> GDH 2279

<400> 66  
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 20 25 30  
 Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val  
 35 40 45  
 Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Gln Gly  
 50 55 60  
 Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile  
 65 70 75 80  
 Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu  
 85 90 95  
 Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val  
 100 105 110  
 Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile  
 115 120 125  
 Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser  
 130 135 140  
 Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala

145		150		155		160									
Ser	Lys	Gly	Gly	Met	Lys	Leu	Met	Thr	Glu	Thr	Leu	Ala	Leu	Glu	Tyr
		165		170		175									
Ala	Pro	Lys	Gly	Ile	Arg	Val	Asn	Asn	Ile	Gly	Pro	Gly	Ala	Ile	Asn
		180		185		190									
Thr	Pro	Ile	Asn	Ala	Glu	Lys	Phe	Ala	Asp	Pro	Lys	Gln	Lys	Ala	Asp
		195		200		205									
Ala	Glu	Ser	Met	Ile	Pro	Met	Gly	Tyr	Ile	Gly	Glu	Pro	Glu	Glu	Ile
	210			215		220									
Ala	Ala	Val	Ala	Ala	Trp	Leu	Ala	Ser	Lys	Glu	Ala	Ser	Tyr	Val	Thr
	225			230		235									240
Gly	Val	Thr	Leu	Phe	Ala	Asp	Gly	Gly	Met	Thr	Gln	Tyr	Pro	Ser	Phe
			245			250								255	
Gln	Ala	Gly	Arg	Gly											
			260												

<210> 67  
 <211> 789  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> GDH 2379

<221> CDS  
 <222> (1)... (789)

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1 5 10 15	
tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag gag cag gca	96
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala	
20 25 30	
aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg aac gag gta	144
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val	
35 40 45	
aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc gtc caa gga	192
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly	
50 55 60	
gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa acg gca att	240
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile	
65 70 75 80	
aag gag ttc ggc aca ctc gat att atg att aat aat gcc ggt ctt gaa	288
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu	
85 90 95	
aat cct gtg cca tct cac gaa atg ccg ctc aag gat tgg gat aaa gtc	336
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val	
100 105 110	
atc ggc acg aac tta acg ggt gcc ttt tta gga agc cgt gaa gcg att	384

Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile	
115 120 125	
aaa tat ttc gta gaa aac gat atc aag gga aat gtc att aac atg tcc	432
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser	
130 135 140	
agt gtg cac gaa gtg att cct tgg ccg tta ttt gtc cac tat gcg gca	480
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala	
145 150 155 160	
agt aaa ggc ggg ctt aag ctg atg aca gaa aca tta gcg ttg gaa tac	528
Ser Lys Gly Gly Leu Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr	
165 170 175	
gcg ccg aag ggc att cgc gtc aat aat att ggg cca ggt gcg atc aac	576
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn	
180 185 190	
acg cca atc aat gct gaa aaa ttc gct gac cct aaa cag aaa gct gat	624
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp	
195 200 205	
gta gaa agc atg att cca atg gga tat atc ggc gaa ccg gag gag atc	672
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile	
210 215 220	
gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc agc tac gtc aca	720
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr	
225 230 235 240	
ggc atc acg tta ttc gcg gac ggc ggt atg aca caa tat cct tca ttc	768
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe	
245 250 255	
cag gca ggc cgc ggt taa tga	789
Gln Ala Gly Arg Gly * *	
260	

<210> 68

<211> 261

<212> PRT

<213> Artificial Sequence

<220>

<223> GDH 2379

<400> 68

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20 25 30	
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val	
35 40 45	
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly	
50 55 60	

Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile  
 65 70 75 80  
 Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu  
 85 90 95  
 Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val  
 100 105 110  
 Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile  
 115 120 125  
 Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser  
 130 135 140  
 Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala  
 145 150 155 160  
 Ser Lys Gly Gly Leu Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr  
 165 170 175  
 Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn  
 180 185 190  
 Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp  
 195 200 205  
 Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile  
 210 215 220  
 Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr  
 225 230 235 240  
 Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe  
 245 250 255  
 Gln Ala Gly Arg Gly  
 260

<210> 69  
 <211> 1206  
 <212> DNA  
 <213> Artificial Sequence

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 <221> CDS  
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 ccg aaa acc tat gca cgt gat gat cta ccg aaa att gat cat tat ccg 96  
 Pro Lys Thr Tyr Ala Arg Asp Asp Leu Pro Lys Ile Asp His Tyr Pro  
 20 25 30  
 ggt ggt cag acc cta ccg acc ccg aaa gca att gat ttt acc ccg ggt 144  
 Gly Gly Gln Thr Leu Pro Thr Pro Lys Ala Ile Asp Phe Thr Pro Gly  
 35 40 45  
 cag cta cta ggt agc gtt agc ggt gaa cta ggt cta cgt aaa tat cta 192  
 Gln Leu Leu Gly Ser Val Ser Gly Glu Leu Gly Leu Arg Lys Tyr Leu  
 50 55 60  
 gaa agc aac ggt cat acc cta gtt gtt acc agc gat aag gac ggc cct 240  
 Glu Ser Asn Gly His Thr Leu Val Val Thr Ser Asp Lys Asp Gly Pro



65	70	75	80	
gac agc gtg ttc gag cgc gag cta gtg gac gcc gac gtg gtg att agc				288
Asp Ser Val Phe Glu Arg Glu Leu Val Asp Ala Asp Val Val Ile Ser	85	90	95	
cag cct ttc tgg cct gcc tat cta acc cct gag cgc att gcc aag gcc				336
Gln Pro Phe Trp Pro Ala Tyr Leu Thr Pro Glu Arg Ile Ala Lys Ala	100	105	110	
aag aat cta aag cta gcc cta acc gcc ggc att ggc agc gac cat gtg				384
Lys Asn Leu Lys Leu Ala Leu Thr Ala Gly Ile Gly Ser Asp His Val	115	120	125	
gac cta cag agc gcc att gac cgc aat gtg acc gtg gcc gag gtg acc				432
Asp Leu Gln Ser Ala Ile Asp Arg Asn Val Thr Val Ala Glu Val Thr	130	135	140	
tat tgt aat agc att agc gtg gcc gag cat gtg gtg atg atg att cta				480
Tyr Cys Asn Ser Ile Ser Val Ala Glu His Val Val Met Met Ile Leu	145	150	155	160
agc cta gtg cgc aat tat cta cct tcc cat gaa tgg gcg cgt aaa ggc				528
Ser Leu Val Arg Asn Tyr Leu Pro Ser His Glu Trp Ala Arg Lys Gly	165	170	175	
ggc tgg aac atc gcg gat tgc gtc tcc cat gcg tat gat ctg gaa gcg				576
Gly Trp Asn Ile Ala Asp Cys Val Ser His Ala Tyr Asp Leu Glu Ala	180	185	190	
atg cat gtc ggc acg gtc gcg gcg ggc cgt atc gcc ctg gcg gtc ctg				624
Met His Val Gly Thr Val Ala Ala Gly Arg Ile Ala Leu Ala Val Leu	195	200	205	
cgt cgt ctg gcg ccg ttt gat gtc cat ctg cat tat acg gat cgt cat				672
Arg Arg Leu Ala Pro Phe Asp Val His Leu His Tyr Thr Asp Arg His	210	215	220	
cgt ctg ccg gaa tgc gta gaa aaa gaa tta aac tta acg tgg cat gcg				720
Arg Leu Pro Glu Ser Val Glu Lys Glu Leu Asn Leu Thr Trp His Ala	225	230	235	240
acg agg gaa gat atg tac cca gta tgt gat gta gta acg tta aac tgt				768
Thr Arg Glu Asp Met Tyr Pro Val Cys Asp Val Val Thr Leu Asn Cys	245	250	255	
cca tta cat cca gaa acg gaa cat atg att aac gat gaa acg tta aaa				816
Pro Leu His Pro Glu Thr Glu His Met Ile Asn Asp Glu Thr Leu Lys	260	265	270	
tta ttc aaa agg gga gcg tac att gtc aac acg gcg aga ggc aaa ttg				864
Leu Phe Lys Arg Gly Ala Tyr Ile Val Asn Thr Ala Arg Gly Lys Leu	275	280	285	
tgc gat aga gat gcg gtc gcg aga gcg ttg gaa tca ggc aga ttg gca				912
Cys Asp Arg Asp Ala Val Ala Arg Ala Leu Glu Ser Gly Arg Leu Ala	290	295	300	

ggc tat gcg ggc gat gtc tgg ttt ccg caa ccg gcg ccg aaa gat cat	960
Gly Tyr Ala Gly Asp Val Trp Phe Pro Gln Pro Ala Pro Lys Asp His	
305 310 315 320	
ccg tgg aga acg atg ccg tat aac ggc atg acg ccg cat att tca ggc	1008
Pro Trp Arg Thr Met Pro Tyr Asn Gly Met Thr Pro His Ile Ser Gly	
325 330 335	
acg acg ttg acg gcg caa gcg aga tat gct gcg ggc acg aga gaa att	1056
Thr Thr Leu Thr Ala Gln Ala Arg Tyr Ala Ala Gly Thr Arg Glu Ile	
340 345 350	
ttg gaa tgc ttt ttt gaa ggc aga cca atc cgt gac gaa tat ctg atc	1104
Leu Glu Cys Phe Phe Glu Gly Arg Pro Ile Arg Asp Glu Tyr Leu Ile	
355 360 365	
gtc cag ggt ggt gcc ctg gcc ggt acc ggt gcc cat tct tat tct aaa	1152
Val Gln Gly Gly Ala Leu Ala Gly Thr Gly Ala His Ser Tyr Ser Lys	
370 375 380	
ggt aat gcc acc ggt ggt tct gaa gaa gcc aaa ttc aaa aaa gcc gtc	1200
Gly Asn Ala Thr Gly Gly Ser Glu Glu Ala Lys Phe Lys Lys Ala Val	
385 390 395 400	
taa tga	1206
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<210> 70  
 <211> 400  
 <212> PRT  
 <213> Pseudomonas sp. strain 101

<400> 70

Met Ala Lys Val Leu Cys Val Leu Tyr Asp Asp Pro Val Asp Gly Tyr	
1 5 10 15	
Pro Lys Thr Tyr Ala Arg Asp Asp Leu Pro Lys Ile Asp His Tyr Pro	
20 25 30	
Gly Gly Gln Thr Leu Pro Thr Pro Lys Ala Ile Asp Phe Thr Pro Gly	
35 40 45	
Gln Leu Leu Gly Ser Val Ser Gly Glu Leu Gly Leu Arg Lys Tyr Leu	
50 55 60	
Glu Ser Asn Gly His Thr Leu Val Val Thr Ser Asp Lys Asp Gly Pro	
65 70 75 80	
Asp Ser Val Phe Glu Arg Glu Leu Val Asp Ala Asp Val Val Ile Ser	
85 90 95	
Gln Pro Phe Trp Pro Ala Tyr Leu Thr Pro Glu Arg Ile Ala Lys Ala	
100 105 110	
Lys Asn Leu Lys Leu Ala Leu Thr Ala Gly Ile Gly Ser Asp His Val	
115 120 125	
Asp Leu Gln Ser Ala Ile Asp Arg Asn Val Thr Val Ala Glu Val Thr	
130 135 140	
Tyr Cys Asn Ser Ile Ser Val Ala Glu His Val Val Met Met Ile Leu	
145 150 155 160	
Ser Leu Val Arg Asn Tyr Leu Pro Ser His Glu Trp Ala Arg Lys Gly	



atc aca aca ccc ttc cac ccc gct tac atc aca aaa gaa aga atc gat Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Ile Asp 65 70 75 80	240
aaa gct aaa aaa ttg aaa ttg gtc gtc gtc gct ggt gtc ggt tcc gat Lys Ala Lys Lys Leu Lys Leu Val Val Val Ala Gly Val Gly Ser Asp 85 90 95	288
cac atc gat ttg gat tac atc aat caa aca ggt aaa aaa atc tcc gtc His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser Val 100 105 110	336
ttg gaa gtc aca ggt tcc aat gtc gtc tcc gtc gct gaa cac gtc gtc Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val Val 115 120 125	384
atg aca atg ttg gtc ttg gtc aga aat ttc gtc ccc gct cac gaa caa Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu Gln 130 135 140	432
atc atc aat cac gat tgg gaa gtc gct gct atc gct aaa gat gct tac Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala Tyr 145 150 155 160	480
gat atc gaa ggt aaa aca atc gct aca atc ggt gct ggt aga atc ggt Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile Gly 165 170 175	528
tac aga gtc ttg gaa aga ttg gtc ccc ttc aat ccc aaa gaa ttg ttg Tyr Arg Val Leu Glu Arg Leu Val Pro Phe Asn Pro Lys Glu Leu Leu 180 185 190	576
tac tac gat tac caa gct ttg ccc aaa gat gct gaa gaa aaa gtt ggt Tyr Tyr Asp Tyr Gln Ala Leu Pro Lys Asp Ala Glu Glu Lys Val Gly 195 200 205	624
gct cgt cgt gtt gaa aac ata gaa gaa ttg gtt gct cag gct gat ata Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp Ile 210 215 220	672
gtt acc gtt aac gct ccg ttg cac gct ggt acc aaa ggt ttg ata aac Val Thr Val Asn Ala Pro Leu His Ala Gly Thr Lys Gly Leu Ile Asn 225 230 235 240	720
aaa gaa ttg ttg tca aaa ttt aaa aaa ggt gct tgg ttg ctt aac acc Lys Glu Leu Leu Ser Lys Phe Lys Lys Gly Ala Trp Leu Leu Asn Thr 245 250 255	768
gct cgt ggt gct ata tgc gtt gct gaa gat gtt gct gct gct ttg gaa Ala Arg Gly Ala Ile Cys Val Ala Glu Asp Val Ala Ala Ala Leu Glu 260 265 270	816
tca ggt cag ttg cgt ggt tac ggt ggt gat gtt tgg ttt ccg cag ccg Ser Gly Gln Leu Arg Gly Tyr Gly Gly Asp Val Trp Phe Pro Gln Pro 275 280 285	864

gct ccg aaa gat cac ccg tgg cgt gat atg cgt aac aaa tac ggt gct	912
Ala Pro Lys Asp His Pro Trp Arg Asp Met Arg Asn Lys Tyr Gly Ala	
290 295 300	
ggt aac gct atg acc ccg cac tac tca ggt acc acc ttg gat gct cag	960
Gly Asn Ala Met Thr Pro His Tyr Ser Gly Thr Thr Leu Asp Ala Gln	
305 310 315 320	
acc cgt tac gct cag ggt acc aaa aac atc ctc gaa tcg ttt ttt acc	1008
Thr Arg Tyr Ala Gln Gly Thr Lys Asn Ile Leu Glu Ser Phe Phe Thr	
325 330 335	
ggt aaa ttt gat tat cgt cca cag gat atc atc ctc ctc aac ggt gaa	1056
Gly Lys Phe Asp Tyr Arg Pro Gln Asp Ile Ile Leu Leu Asn Gly Glu	
340 345 350	
tat gtt acc aaa gcc tat ggt aaa cac gat aaa aaa taa tga	1098
Tyr Val Thr Lys Ala Tyr Gly Lys His Asp Lys Lys * *	
355 360	

<210> 72

<211> 364

<212> PRT

<213> Candida boidinii

<400> 72

Met Lys Ile Val Leu Val Leu Tyr Asp Ala Gly Lys His Ala Ala Asp	
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Glu Glu Lys Leu Tyr Gly Cys Thr Glu Asn Lys Leu Gly Ile Ala Asn	
20 25 30	
Trp Leu Lys Asp Gln Gly His Glu Leu Ile Thr Thr Ser Asp Lys Glu	
35 40 45	
Gly Gly Asn Ser Val Leu Asp Gln His Ile Pro Asp Ala Asp Ile Ile	
50 55 60	
Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Ile Asp	
65 70 75 80	
Lys Ala Lys Lys Leu Lys Leu Val Val Val Ala Gly Val Gly Ser Asp	
85 90 95	
His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser Val	
100 105 110	
Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val Val	
115 120 125	
Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu Gln	
130 135 140	
Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala Tyr	
145 150 155 160	
Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile Gly	
165 170 175	
Tyr Arg Val Leu Glu Arg Leu Val Pro Phe Asn Pro Lys Glu Leu Leu	
180 185 190	
Tyr Tyr Asp Tyr Gln Ala Leu Pro Lys Asp Ala Glu Glu Lys Val Gly	
195 200 205	
Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp Ile	
210 215 220	
Val Thr Val Asn Ala Pro Leu His Ala Gly Thr Lys Gly Leu Ile Asn	
225 230 235 240	



aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
ttc atc act tcg gct gct ccg ttc ggg cca tgg aag gag cta tcg act	432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
tac act tcg gct cga gct ggg gct tgt tcc cta gct aat gct cta tcg	480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Ser Leu Ala Asn Ala Leu Ser	
145 150 155 160	
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp	
180 185 190	
aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta	624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg	672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu	
210 215 220	
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca	720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala	
225 230 235 240	
ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa	765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *	
245 250	

<210> 74  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HHDH P016514-B-12

<400> 74  
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 20 25 30  
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr  
 35 40 45  
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu  
 50 55 60  
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp  
 65 70 75 80  
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp





tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
ttc atc act tcg gct act ccg ttc ggg ccg tgg aag gag cta tcg act	432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg	480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser	
145 150 155 160	
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp	
180 185 190	
aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta	624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg	672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu	
210 215 220	
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca	720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala	
225 230 235 240	
ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa	765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *	
245 250	

<210> 76

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> HHDH Mz1/4H6

<400> 76

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20 25 30	
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	

Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu  
 50 55 60  
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp  
 65 70 75 80  
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp  
 85 90 95  
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val  
 100 105 110  
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile  
 115 120 125  
 Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr  
 130 135 140  
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser  
 145 150 155 160  
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn  
 165 170 175  
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp  
 180 185 190  
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu  
 195 200 205  
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu  
 210 215 220  
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala  
 225 230 235 240  
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  
 245 250

<210> 77  
 <211> 765  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HHDH P016229-F-04

<221> CDS  
 <222> (1)...(765)

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 agt gct ctg agg ctg tcg gag gct ggt cac acc gtc gct tgc cat gat 96  
 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp  
 20 25 30  
 gaa agc ttt aaa cag aaa gat gaa ctg gag gct ttt gct gaa acc tac 144  
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr  
 35 40 45  
 cca cag ctg aaa cca atg agc gaa cag gaa cca gct gga ctg att gaa 192  
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Gly Leu Ile Glu  
 50 55 60  
 gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat 240  
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp

65	70	75	80	
atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat				288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp	85	90	95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg				336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	100	105	110	
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc				384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	115	120	125	
ttc atc act tcg gct act ccg ttc ggg cca tgg aag gag cta tcg act				432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	130	135	140	
tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg				480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser	145	150	155	160
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat				528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	165	170	175	
tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg				576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp	180	185	190	
aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta				624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	195	200	205	
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg				672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu	210	215	220	
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca				720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala	225	230	235	240
ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa				765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *	245	250		

<210> 78

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> HHDH P016229-F-04

<400> 78

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	20	25	30
Glu Ser Phe Lys	Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr		
	35	40	45
Pro Gln Leu Lys	Pro Met Ser Glu Gln Glu Pro Ala Gly Leu Ile Glu		
	50	55	60
Ala Val Thr Ser	Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp		
65		70	75
Ile Phe Ala Pro	Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp		
	85	90	95
Tyr Arg Gly Ala	Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val		
	100	105	110
Asn Ala Val Ala	Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile		
	115	120	125
Phe Ile Thr Ser	Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr		
	130	135	140
Tyr Thr Ser Ala	Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser		
145		150	155
Lys Glu Leu Gly	Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn		
	165	170	175
Tyr Leu His Ser	Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp		
	180	185	190
Lys Thr Asn Pro	Glu His Val Ala His Val Lys Lys Val Thr Ala Leu		
	195	200	205
Gln Arg Leu Gly	Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu		
	210	215	220
Ala Ser Gly Ser	Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala		
225		230	235
Gly Gly Phe Pro	Met Ile Glu Arg Trp Pro Gly Met Pro Glu		
	245	250	

<210> 79  
 <211> 765  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HHDH P016230-A-08

<221> CDS  
 <222> (1)...(765)

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1 5 10 15	
agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat	96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	
gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac	144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa	192

Pro	Gln	Leu	Lys	Pro	Met	Ser	Glu	Gln	Glu	Pro	Ala	Glu	Leu	Ile	Glu		
50						55					60						
gct	gtc	acc	agc	gct	tac	ggc	cag	gtc	gat	gtc	ctg	gtc	agc	aac	gat	240	
Ala	Val	Thr	Ser	Ala	Tyr	Gly	Gln	Val	Asp	Val	Leu	Val	Ser	Asn	Asp		
65					70				75						80		
atc	ttt	gct	cca	gaa	ttt	cag	cca	atc	gat	aaa	tac	gct	gtc	gaa	gat	288	
Ile	Phe	Ala	Pro	Glu	Phe	Gln	Pro	Ile	Asp	Lys	Tyr	Ala	Val	Glu	Asp		
				85					90					95			
tat	cgt	ggc	gct	gtc	gaa	gct	ctg	cag	atc	agg	cca	ttt	gct	cta	gtg	336	
Tyr	Arg	Gly	Ala	Val	Glu	Ala	Leu	Gln	Ile	Arg	Pro	Phe	Ala	Leu	Val		
			100					105					110				
aat	gct	gtg	gct	tcg	caa	atg	aag	aag	cga	aag	tcg	ggg	cac	atc	atc	384	
Asn	Ala	Val	Ala	Ser	Gln	Met	Lys	Lys	Arg	Lys	Ser	Gly	His	Ile	Ile		
		115					120					125					
ttc	atc	act	tcg	gct	act	ccg	ttc	ggg	cca	tgg	aag	gag	cta	tcg	act	432	
Phe	Ile	Thr	Ser	Ala	Thr	Pro	Phe	Gly	Pro	Trp	Lys	Glu	Leu	Ser	Thr		
	130					135					140						
tac	act	tcg	gct	cga	gct	ggg	gct	tgt	act	cta	gct	aat	gct	cta	tcg	480	
Tyr	Thr	Ser	Ala	Arg	Ala	Gly	Ala	Cys	Thr	Leu	Ala	Asn	Ala	Leu	Ser		
145					150					155					160		
aag	gag	cta	gga	gag	tac	aat	atc	ccg	gtg	ttc	gct	atc	ggg	ccg	aat	528	
Lys	Glu	Leu	Gly	Glu	Tyr	Asn	Ile	Pro	Val	Phe	Ala	Ile	Gly	Pro	Asn		
			165					170					175				
tac	cta	cac	tcg	gag	gat	tcg	ccg	tac	ttc	tac	ccg	act	gag	ccg	tgg	576	
Tyr	Leu	His	Ser	Glu	Asp	Ser	Pro	Tyr	Phe	Tyr	Pro	Thr	Glu	Pro	Trp		
			180					185					190				
aag	act	aat	ccg	gaa	cac	gtg	gct	cac	gtg	aag	aag	gtg	act	gct	cta	624	
Lys	Thr	Asn	Pro	Glu	His	Val	Ala	His	Val	Lys	Lys	Val	Thr	Ala	Leu		
		195					200					205					
caa	cga	cta	ggg	act	caa	aaa	gag	ttg	ggg	gaa	ttg	gtg	gca	ttt	ttg	672	
Gln	Arg	Leu	Gly	Thr	Gln	Lys	Glu	Leu	Gly	Glu	Leu	Val	Ala	Phe	Leu		
	210					215					220						
gca	tct	ggc	tct	tgt	gat	tat	ttg	act	ggc	cag	gtg	ttt	tgg	ttg	gca	720	
Ala	Ser	Gly	Ser	Cys	Asp	Tyr	Leu	Thr	Gly	Gln	Val	Phe	Trp	Leu	Ala		
225					230				235						240		
ggc	ggc	ttt	ccc	atg	ata	gaa	cgt	tgg	ccc	ggc	atg	ccc	gaa	taa		765	
Gly	Gly	Phe	Pro	Met	Ile	Glu	Arg	Trp	Pro	Gly	Met	Pro	Glu	*			
			245					250									

<210> 80  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> HHDH P016230-A-08

<400> 80

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Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1          5          10          15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
      20          25          30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
      35          40          45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
      50          55          60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65          70          75          80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
      85          90          95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
      100          105          110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
      115          120          125
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
      130          135          140
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145          150          155          160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
      165          170          175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
      180          185          190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
      195          200          205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
      210          215          220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225          230          235          240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
      245          250
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<210> 81

<211> 765

<212> DNA

<213> Artificial Sequence

<220>

<223> HHDH P016096-G9

<221> CDS

<222> (1)... (765)

<400> 81

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Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1          5          10          15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat      96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
      20          25          30
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gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac	144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa	192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat	288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
ttc atc act tcg gct act ccg ttc ggg cca tgg aaa gag cta tcg act	432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg	480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser	
145 150 155 160	
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp	
180 185 190	
aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta	624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttc ctg	672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu	
210 215 220	
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca	720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala	
225 230 235 240	
ggc ggc ttt ccc att atc gaa cgt tgg ccc ggc atg ccc gaa taa	765
Gly Gly Phe Pro Ile Ile Glu Arg Trp Pro Gly Met Pro Glu *	
245 250	

<210> 82  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HHDH P016096-G9

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 20 25 30  
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr  
 35 40 45  
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu  
 50 55 60  
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp  
 65 70 75 80  
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp  
 85 90 95  
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val  
 100 105 110  
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile  
 115 120 125  
 Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr  
 130 135 140  
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser  
 145 150 155 160  
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn  
 165 170 175  
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp  
 180 185 190  
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu  
 195 200 205  
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu  
 210 215 220  
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala  
 225 230 235 240  
 Gly Gly Phe Pro Ile Ile Glu Arg Trp Pro Gly Met Pro Glu  
 245 250

<210> 83  
 <211> 765  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HHDH P016097-F9

<221> CDS  
 <222> (1)... (765)

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 Met Thr Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly  
 1 5 10 15



agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp 20 25 30	96
gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr 35 40 45	144
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu 50 55 60	192
gct gtc acc agc gct tac ggt cag gtc gat atc ctg gtc agc aac gat Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Ile Leu Val Ser Asn Asp 65 70 75 80	240
atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc cag gat Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp 85 90 95	288
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val 100 105 110	336
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile 115 120 125	384
ttc atc act tcg gct gct ccg ttc ggg cca tgg aag gag cta tcg act Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr 130 135 140	432
tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser 145 150 155 160	480
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn 165 170 175	528
tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp 180 185 190	576
aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu 195 200 205	624
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu 210 215 220	672
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala 225 230 235 240	720

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa  
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu \*  
 245 250

765

<210> 84  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HHDH P016097-F9

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 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp  
 20 25 30  
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 35 40 45  
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu  
 50 55 60  
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Ile Leu Val Ser Asn Asp  
 65 70 75 80  
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp  
 85 90 95  
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val  
 100 105 110  
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile  
 115 120 125  
 Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr  
 130 135 140  
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser  
 145 150 155 160  
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn  
 165 170 175  
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp  
 180 185 190  
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu  
 195 200 205  
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu  
 210 215 220  
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala  
 225 230 235 240  
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  
 245 250

<210> 85  
 <211> 765  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HHDH P016097-H10

<221> CDS  
 <222> (1)...(765)

<400> 85

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agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat	96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac	144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa	192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	

gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc cag gat	288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp	
85 90 95	

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	

ttc atc act tcg gct gct ccg ttc ggg cca tgg aag gag cta tcg act	432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	

tac act tcg gct cga gct ggg gct tgt tcc cta gct aat gct cta tcg	480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Ser Leu Ala Asn Ala Leu Ser	
145 150 155 160	

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp	
180 185 190	

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta	624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg	672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu	
210 215 220	

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca 720  
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala  
 225 230 235 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa 765  
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu \*  
 245 250

<210> 86  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HHDH P016097-H10

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 35 40 45  
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu  
 50 55 60  
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp  
 65 70 75 80  
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp  
 85 90 95  
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val  
 100 105 110  
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile  
 115 120 125  
 Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr  
 130 135 140  
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Ser Leu Ala Asn Ala Leu Ser  
 145 150 155 160  
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn  
 165 170 175  
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp  
 180 185 190  
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu  
 195 200 205  
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu  
 210 215 220  
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala  
 225 230 235 240  
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  
 245 250

<210> 87  
 <211> 765  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> HHDH P016099-A1

<221> CDS

<222> (1)...(765)

<400> 87

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agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat	96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	
gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac	144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa	192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
gct gtc acc agc gct tac ggt cag gtc gat atc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Ile Leu Val Ser Asn Asp	
65 70 75 80	
atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc cag gat	288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp	
85 90 95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
ttc atc act tcg gct gct ccg ttc ggg cca tgg aag gag cta tcg act	432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg	480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser	
145 150 155 160	
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp	
180 185 190	
aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta	624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	

195	200	205	
caa cga cta ggg act	caa aaa gag ttg ggg	gaa ttg gtg gca ttt ttg	672
Gln Arg Leu Gly Thr	Gln Lys Glu Leu Gly	Glu Leu Val Ala Phe Leu	
210	215	220	
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca			720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala			
225	230	235	240
ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa			765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *			
245	250		

<210> 88  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HHDH P016099-A1

<400> 88

Met Thr Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly	
1 5 10 15	
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Ile Leu Val Ser Asn Asp	
65 70 75 80	
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp	
85 90 95	
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser	
145 150 155 160	
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp	
180 185 190	
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu	
210 215 220	
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala	
225 230 235 240	
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu	
245 250	

<210> 89  
 <211> 765  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HHDH P016231-A-03

<221> CDS  
 <222> (1)...(765)

<400> 89  
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 1 5 10 15  
 agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat 96  
 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp  
 20 25 30  
 gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac 144  
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr  
 35 40 45  
 cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa 192  
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu  
 50 55 60  
 gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat 240  
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp  
 65 70 75 80  
 atc ttt gct tca gaa ttt cag cca atc gat aaa tac gcc gtc gaa gat 288  
 Ile Phe Ala Ser Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp  
 85 90 95  
 tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg 336  
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val  
 100 105 110  
 aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc 384  
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile  
 115 120 125  
 ttc atc act tcg gct act ccg ttc ggg cca tgg aag gag cta tcg act 432  
 Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr  
 130 135 140  
 tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg 480  
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser  
 145 150 155 160  
 aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat 528  
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn  
 165 170 175  
 tat cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg 576

Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp  
 180 185 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta 624  
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu  
 195 200 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg 672  
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu  
 210 215 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca 720  
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala  
 225 230 235 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa 765  
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu \*  
 245 250

<210> 90  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HHDH P016231-A-03

<400> 90  
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 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp  
 20 25 30  
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr  
 35 40 45  
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu  
 50 55 60  
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp  
 65 70 75 80  
 Ile Phe Ala Ser Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp  
 85 90 95  
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val  
 100 105 110  
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile  
 115 120 125  
 Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr  
 130 135 140  
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser  
 145 150 155 160  
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn  
 165 170 175  
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp  
 180 185 190  
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu  
 195 200 205  
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu  
 210 215 220



Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala  
 225 230 235 240  
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  
 245 250

<210> 91  
 <211> 765  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HHDH P016231-E-03

<221> CDS  
 <222> (1)...(765)

<400> 91  
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 1 5 10 15  
 agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat 96  
 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp  
 20 25 30  
 gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac 144  
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr  
 35 40 45  
 cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa 192  
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu  
 50 55 60  
 gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat 240  
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp  
 65 70 75 80  
 atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat 288  
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp  
 85 90 95  
 tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg 336  
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val  
 100 105 110  
 aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc 384  
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile  
 115 120 125  
 ttc atc act tcg gct act ccg ttc ggg cca tgg aag gag cta tcg act 432  
 Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr  
 130 135 140  
 tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg 480  
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser  
 145 150 155 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
tac cta cac tcg gag gat tcg ccg tac tat tat ccg act gag ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp	
180 185 190	
aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta	624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg	672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu	
210 215 220	
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca	720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala	
225 230 235 240	
ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa	765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *	
245 250	

<210> 92  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HHDH P016231-E-03

<400> 92

Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly	
1 5 10 15	
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser	
145 150 155 160	
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp	

			180						185					190			
Lys	Thr	Asn	Pro	Glu	His	Val	Ala	His	Val	Lys	Lys	Val	Thr	Ala	Leu		
		195					200					205					
Gln	Arg	Leu	Gly	Thr	Gln	Lys	Glu	Leu	Gly	Glu	Leu	Val	Ala	Phe	Leu		
	210					215					220						
Ala	Ser	Gly	Ser	Cys	Asp	Tyr	Leu	Thr	Gly	Gln	Val	Phe	Trp	Leu	Ala		
225					230					235					240		
Gly	Gly	Phe	Pro	Met	Ile	Glu	Arg	Trp	Pro	Gly	Met	Pro	Glu				
			245						250								

<210> 93

<211> 765

<212> DNA

<213> Artificial Sequence

<220>

<223> HHDH S00827801

<221> CDS

<222> (1)...(765)

<400> 93

atg	agc	acc	gct	atc	gtc	acc	aac	gtc	aaa	cat	ttt	gga	ggt	atg	ggt		48
Met	Ser	Thr	Ala	Ile	Val	Thr	Asn	Val	Lys	His	Phe	Gly	Gly	Met	Gly		
1				5					10					15			

agc	gct	ctg	agg	ctg	agc	gaa	ggt	ggt	cat	acc	gtc	gct	tgc	cat	gat		96
Ser	Ala	Leu	Arg	Leu	Ser	Glu	Gly	Gly	His	Thr	Val	Ala	Cys	His	Asp		
			20					25					30				

gaa	agc	ttt	aaa	cag	aaa	gat	gaa	ctg	gaa	gct	ttt	gct	gaa	acc	tac		144
Glu	Ser	Phe	Lys	Gln	Lys	Asp	Glu	Leu	Glu	Ala	Phe	Ala	Glu	Thr	Tyr		
		35					40					45					

cca	cag	ctg	aaa	cca	atg	agc	gaa	cag	gaa	cca	gct	gaa	ctg	atc	gaa		192
Pro	Gln	Leu	Lys	Pro	Met	Ser	Glu	Gln	Glu	Pro	Ala	Glu	Leu	Ile	Glu		
	50					55					60						

gct	gtc	acc	agc	gct	ttt	ggt	cag	gtc	gat	gtc	ctg	gtc	agc	aac	gat		240
Ala	Val	Thr	Ser	Ala	Phe	Gly	Gln	Val	Asp	Val	Leu	Val	Ser	Asn	Asp		
65					70				75						80		

atc	ttt	gct	cca	gaa	ttt	cag	cca	atc	gat	aaa	tac	gct	gtc	gaa	gat		288
Ile	Phe	Ala	Pro	Glu	Phe	Gln	Pro	Ile	Asp	Lys	Tyr	Ala	Val	Glu	Asp		
				85					90					95			

tac	agg	ggt	gct	gtc	gaa	gct	ctg	cag	atc	agg	cca	ttt	gct	cta	gtg		336
Tyr	Arg	Gly	Ala	Val	Glu	Ala	Leu	Gln	Ile	Arg	Pro	Phe	Ala	Leu	Val		
			100					105					110				

aat	gct	gtg	gct	tcg	caa	atg	aag	aag	cga	aag	tcg	ggg	cac	atc	atc		384
Asn	Ala	Val	Ala	Ser	Gln	Met	Lys	Lys	Arg	Lys	Ser	Gly	His	Ile	Ile		
		115					120					125					

ttc	atc	act	tcg	gct	gcc	ccg	ttc	ggg	cca	tgg	aag	gag	cta	tcg	act		432
Phe	Ile	Thr	Ser	Ala	Ala	Pro	Phe	Gly	Pro	Trp	Lys	Glu	Leu	Ser	Thr		
	130					135					140						

tac	act	tcg	gct	cga	gct	ggg	gct	agt	act	cta	gct	aat	gct	cta	tcg	480
Tyr	Thr	Ser	Ala	Arg	Ala	Gly	Ala	Ser	Thr	Leu	Ala	Asn	Ala	Leu	Ser	
145					150					155					160	

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg 576  
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp  
180 185 190

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg 672  
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu  
210 215 220

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa 765  
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu \*  
245 250

<220>  
<223> HHDH S00827801

Tyr	Thr	Ser	Ala	Arg	Ala	Gly	Ala	Ser	Thr	Leu	Ala	Asn	Ala	Leu	Ser
145					150					155				160	
Lys	Glu	Leu	Gly	Glu	Tyr	Asn	Ile	Pro	Val	Phe	Ala	Ile	Gly	Pro	Asn
			165						170					175	
Tyr	Leu	His	Ser	Glu	Asp	Ser	Pro	Tyr	Phe	Tyr	Pro	Thr	Glu	Pro	Trp
		180					185						190		
Lys	Thr	Asn	Pro	Glu	His	Val	Ala	His	Val	Lys	Lys	Val	Thr	Ala	Leu
	195					200						205			
Gln	Arg	Leu	Gly	Thr	Gln	Lys	Glu	Leu	Gly	Glu	Leu	Val	Ala	Phe	Leu
	210				215					220					
Ala	Ser	Gly	Ser	Cys	Asp	Tyr	Leu	Thr	Gly	Gln	Val	Phe	Trp	Leu	Ala
225				230					235					240	
Gly	Gly	Phe	Pro	Met	Ile	Glu	Arg	Trp	Pro	Gly	Met	Pro	Glu		
			245					250							

<210> 95

<211> 765

<212> DNA

<213> Artificial Sequence

<220>

<223> HHDH S00890554

<221> CDS

<222> (1)...(765)

<400> 95

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Met	Ser	Thr	Ala	Ile	Val	Thr	Asn	Val	Lys	His	Phe	Gly	Gly	Met	Gly	
1			5					10					15			

agc	gct	ctg	agg	ctg	agc	gaa	gct	ggt	cat	acc	gtc	gct	tgc	cat	gat	96
Ser	Ala	Leu	Arg	Leu	Ser	Glu	Ala	Gly	His	Thr	Val	Ala	Cys	His	Asp	
		20					25					30				

gaa	agc	ttt	aaa	cag	aaa	gat	gaa	ctg	gaa	gct	ttt	gct	gaa	acc	tac	144
Glu	Ser	Phe	Lys	Gln	Lys	Asp	Glu	Leu	Glu	Ala	Phe	Ala	Glu	Thr	Tyr	
	35					40					45					

cca	cag	ctg	aaa	cca	atg	agc	gaa	cag	gaa	cca	gct	gaa	ctg	atc	gaa	192
Pro	Gln	Leu	Lys	Pro	Met	Ser	Glu	Gln	Glu	Pro	Ala	Glu	Leu	Ile	Glu	
	50					55				60						

gct	gtc	acc	agc	gct	ttt	ggt	cag	gtc	gat	gtc	ctg	gtc	agc	aac	gat	240
Ala	Val	Thr	Ser	Ala	Phe	Gly	Gln	Val	Asp	Val	Leu	Val	Ser	Asn	Asp	
	65			70				75					80			

atc	ttt	gct	cta	gaa	ttt	cag	cca	atc	gat	aaa	tac	gct	gtc	gaa	gat	288
Ile	Phe	Ala	Leu	Glu	Phe	Gln	Pro	Ile	Asp	Lys	Tyr	Ala	Val	Glu	Asp	
		85						90					95			

tac	agg	ggt	gct	gtc	gaa	gct	ctg	cag	atc	agg	cca	ttt	gct	cta	gtg	336
Tyr	Arg	Gly	Ala	Val	Glu	Ala	Leu	Gln	Ile	Arg	Pro	Phe	Ala	Leu	Val	
		100					105				110					

aat	gct	gtg	gct	tcg	caa	atg	aag	aag	cga	aag	tcg	ggg	cac	atc	atc	384
Asn	Ala	Val	Ala	Ser	Gln	Met	Lys	Lys	Arg	Lys	Ser	Gly	His	Ile	Ile	

115	120	125	
ttc atc act tcg gct gcc ccg ttc ggg cca tgg aag gag cta tcg act			432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr			
130	135	140	
tac act tcg gct cga gct ggg gct agt act cta gct aat gct cta tcg			480
Tyr Thr Ser Ala Arg Ala Gly Ala Ser Thr Leu Ala Asn Ala Leu Ser			
145	150	155 160	
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat			528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn			
165	170	175	
tac cta cac tcg gag gat tcg ccg tac tat tac ccc act gag ccg tgg			576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp			
180	185	190	
aag att aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta			624
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu			
195	200	205	
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg			672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu			
210	215	220	
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca			720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala			
225	230	235 240	
ggc ggc ttt ccc acg ata gaa cgt tgg ccc ggc atg ccc gaa taa			765
Gly Gly Phe Pro Thr Ile Glu Arg Trp Pro Gly Met Pro Glu *			
245	250		

<210> 96

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> HHDH S00890554

<400> 96

Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly	
1 5 10 15	
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
Ile Phe Ala Leu Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	

	100		105		110										
Asn	Ala	Val	Ala	Ser	Gln	Met	Lys	Lys	Arg	Lys	Ser	Gly	His	Ile	Ile
	115						120					125			
Phe	Ile	Thr	Ser	Ala	Ala	Pro	Phe	Gly	Pro	Trp	Lys	Glu	Leu	Ser	Thr
	130						135					140			
Tyr	Thr	Ser	Ala	Arg	Ala	Gly	Ala	Ser	Thr	Leu	Ala	Asn	Ala	Leu	Ser
	145					150				155				160	
Lys	Glu	Leu	Gly	Glu	Tyr	Asn	Ile	Pro	Val	Phe	Ala	Ile	Gly	Pro	Asn
			165						170					175	
Tyr	Leu	His	Ser	Glu	Asp	Ser	Pro	Tyr	Tyr	Tyr	Pro	Thr	Glu	Pro	Trp
		180						185					190		
Lys	Ile	Asn	Pro	Glu	His	Val	Ala	His	Val	Lys	Lys	Val	Thr	Ala	Leu
	195						200					205			
Gln	Arg	Leu	Gly	Thr	Gln	Lys	Glu	Leu	Gly	Glu	Leu	Val	Ala	Phe	Leu
	210					215					220				
Ala	Ser	Gly	Ser	Cys	Asp	Tyr	Leu	Thr	Gly	Gln	Val	Phe	Trp	Leu	Ala
	225				230					235					240
Gly	Gly	Phe	Pro	Thr	Ile	Glu	Arg	Trp	Pro	Gly	Met	Pro	Glu		
			245						250						

<210> 97  
 <211> 765  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HHDH S00994580

<221> CDS  
 <222> (1)...(765)

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atg agc acc gct att gtc acc aac gtc aaa cat ttt gga ggt atg ggt	48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly	
1 5 10 15	
agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat	96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	
gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac	144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg att gaa	192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
gct gtc acc agc gct ttt ggt cag gtc gat gtc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
atc ttt gct cta gaa ttt cag cca atc gat aaa tac gct gtc gaa gat	288
Ile Phe Ala Leu Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg	336

Tyr	Arg	Gly	Ala	Val	Glu	Ala	Leu	Gln	Ile	Arg	Pro	Phe	Ala	Leu	Val		
			100					105					110				
aat	gct	gtg	gct	tcg	caa	atg	aag	aag	cga	aag	tcg	ggg	cac	atc	atc	384	
Asn	Ala	Val	Ala	Ser	Gln	Met	Lys	Lys	Arg	Lys	Ser	Gly	His	Ile	Ile		
		115					120					125					
ttc	atc	act	tcg	gct	gcc	ccg	ttc	ggg	cca	tgg	aag	gag	cta	tcg	act	432	
Phe	Ile	Thr	Ser	Ala	Ala	Pro	Phe	Gly	Pro	Trp	Lys	Glu	Leu	Ser	Thr		
		130				135					140						
tac	act	tcg	gct	cga	gct	ggg	gct	agt	act	cta	gct	aat	gct	cta	tcg	480	
Tyr	Thr	Ser	Ala	Arg	Ala	Gly	Ala	Ser	Thr	Leu	Ala	Asn	Ala	Leu	Ser		
		145			150					155					160		
aag	gag	cta	gga	gag	tac	aat	atc	ccg	gtg	ttc	gct	atc	ggg	ccg	aat	528	
Lys	Glu	Leu	Gly	Glu	Tyr	Asn	Ile	Pro	Val	Phe	Ala	Ile	Gly	Pro	Asn		
			165					170					175				
tac	cta	cac	tcg	gag	gat	tcg	ccg	tac	tat	tac	ccc	act	gag	ccg	tgg	576	
Tyr	Leu	His	Ser	Glu	Asp	Ser	Pro	Tyr	Tyr	Tyr	Pro	Thr	Glu	Pro	Trp		
			180					185					190				
aag	att	aat	ccg	gag	cac	gtg	gct	cac	gtg	aag	aag	gtg	act	gct	cta	624	
Lys	Ile	Asn	Pro	Glu	His	Val	Ala	His	Val	Lys	Lys	Val	Thr	Ala	Leu		
		195				200						205					
caa	cga	cta	ggg	act	caa	aaa	gag	ttg	ggg	gaa	ttg	gtg	gca	ttt	ttg	672	
Gln	Arg	Leu	Gly	Thr	Gln	Lys	Glu	Leu	Gly	Glu	Leu	Val	Ala	Phe	Leu		
		210				215					220						
gca	tct	ggc	tct	tgt	gat	tat	ttg	act	ggc	cag	gtg	ttt	tgg	ttg	gca	720	
Ala	Ser	Gly	Ser	Cys	Asp	Tyr	Leu	Thr	Gly	Gln	Val	Phe	Trp	Leu	Ala		
		225			230				235						240		
ggc	ggc	ttt	ccc	acg	ata	gaa	cgt	tgg	ccc	ggc	atg	ccc	gaa	taa		765	
Gly	Gly	Phe	Pro	Thr	Ile	Glu	Arg	Trp	Pro	Gly	Met	Pro	Glu	*			
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<210> 98

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> HHDH S00994580

<400> 98

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			20					25					30				
Glu	Ser	Phe	Lys	Gln	Lys	Asp	Glu	Leu	Glu	Ala	Phe	Ala	Glu	Thr	Tyr		
		35				40					45						
Pro	Gln	Leu	Lys	Pro	Met	Ser	Glu	Gln	Glu	Pro	Ala	Glu	Leu	Ile	Glu		
		50				55					60						



Ala	Val	Thr	Ser	Ala	Phe	Gly	Gln	Val	Asp	Val	Leu	Val	Ser	Asn	Asp
65					70				75					80	
Ile	Phe	Ala	Leu	Glu	Phe	Gln	Pro	Ile	Asp	Lys	Tyr	Ala	Val	Glu	Asp
			85						90					95	
Tyr	Arg	Gly	Ala	Val	Glu	Ala	Leu	Gln	Ile	Arg	Pro	Phe	Ala	Leu	Val
			100						105					110	
Asn	Ala	Val	Ala	Ser	Gln	Met	Lys	Lys	Arg	Lys	Ser	Gly	His	Ile	Ile
		115					120					125			
Phe	Ile	Thr	Ser	Ala	Ala	Pro	Phe	Gly	Pro	Trp	Lys	Glu	Leu	Ser	Thr
	130					135					140				
Tyr	Thr	Ser	Ala	Arg	Ala	Gly	Ala	Ser	Thr	Leu	Ala	Asn	Ala	Leu	Ser
145					150					155				160	
Lys	Glu	Leu	Gly	Glu	Tyr	Asn	Ile	Pro	Val	Phe	Ala	Ile	Gly	Pro	Asn
			165						170					175	
Tyr	Leu	His	Ser	Glu	Asp	Ser	Pro	Tyr	Tyr	Tyr	Pro	Thr	Glu	Pro	Trp
			180					185					190		
Lys	Ile	Asn	Pro	Glu	His	Val	Ala	His	Val	Lys	Lys	Val	Thr	Ala	Leu
		195					200					205			
Gln	Arg	Leu	Gly	Thr	Gln	Lys	Glu	Leu	Gly	Glu	Leu	Val	Ala	Phe	Leu
	210					215					220				
Ala	Ser	Gly	Ser	Cys	Asp	Tyr	Leu	Thr	Gly	Gln	Val	Phe	Trp	Leu	Ala
225					230					235				240	
Gly	Gly	Phe	Pro	Thr	Ile	Glu	Arg	Trp	Pro	Gly	Met	Pro	Glu		
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<210> 99  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HHDH S01018044

<221> CDS  
 <222> (1)...(765)

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Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly	
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agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat	96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	
gaa agc ttt aag cat aaa gat gaa ctg gaa gct ttt gct gaa acc tac	144
Glu Ser Phe Lys His Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa	192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
gct gtc acc agc gct ttt ggt cag gtc gat gtc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	

atc ttt gct cta gaa ttt cgg cca atc gat aaa tac gct gtc gag gat	288
Ile Phe Ala Leu Glu Phe Arg Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
ttc atc act tcg gct gcc ccg ttc ggg cca tgg aag gag cta tcg act	432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
tac tct tcg gct cga gct ggg gct agt gca cta gct aat gct cta tcg	480
Tyr Ser Ser Ala Arg Ala Gly Ala Ser Ala Leu Ala Asn Ala Leu Ser	
145 150 155 160	
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
tac cta cac tcg gag gat tcg ccg tac tat tac ccc act gag ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp	
180 185 190	
aag att aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta	624
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg	672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu	
210 215 220	
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca	720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala	
225 230 235 240	
ggc ggc ttt ccc gtc ata gaa cgt tgg ccc ggc atg ccc gaa taa	765
Gly Gly Phe Pro Val Ile Glu Arg Trp Pro Gly Met Pro Glu *	
245 250	

<210> 100  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HHDH S0108044

<400> 100  
 Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly  
 1 5 10 15  
 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp



gct gtc acc agc gct ttt ggt cag gtc gat gtc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
atc ttt gct cta gaa ttt cgg cca atc gat aaa tac gct gtc gag gat	288
Ile Phe Ala Leu Glu Phe Arg Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
ttc atc act tcg gct gcc ccg ttc ggg cca tgg aag gag cta tcg act	432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
tac tct tcg gct cga gct ggg gct agt gca cta gct aat gct cta tcg	480
Tyr Ser Ser Ala Arg Ala Gly Ala Ser Ala Leu Ala Asn Ala Leu Ser	
145 150 155 160	
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
tac cta cac tcg gag gat tcg ccg tac tat tac ccc act gag ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp	
180 185 190	
aag att aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta	624
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg	672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu	
210 215 220	
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca	720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala	
225 230 235 240	
ggc ggc ttt ccc gtc ata gaa cgt tgg ccc ggc atg ccc gaa taa	765
Gly Gly Phe Pro Val Ile Glu Arg Trp Pro Gly Met Pro Glu *	
245 250	

<210> 102  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HHDH S01035939

<400> 102

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Ser	Ala	Leu	Arg	Leu	Ser	Glu	Ala	Gly	His	Thr	Val	Ala	Cys	His	Asp
			20					25					30		
Glu	Ser	Phe	Lys	His	Lys	Asp	Glu	Leu	Glu	Ala	Phe	Ala	Glu	Thr	Tyr
		35				40					45				
Pro	Gln	Leu	Lys	Pro	Met	Ser	Glu	Gln	Glu	Pro	Ala	Glu	Leu	Ile	Glu
	50					55					60				
Ala	Val	Thr	Ser	Ala	Phe	Gly	Gln	Val	Asp	Val	Leu	Val	Ser	Asn	Asp
65					70					75				80	
Ile	Phe	Ala	Leu	Glu	Phe	Arg	Pro	Ile	Asp	Lys	Tyr	Ala	Val	Glu	Asp
				85					90					95	
Tyr	Arg	Gly	Ala	Val	Glu	Ala	Leu	Gln	Ile	Arg	Pro	Phe	Ala	Leu	Val
			100					105					110		
Asn	Ala	Val	Ala	Ser	Gln	Met	Lys	Lys	Arg	Lys	Ser	Gly	His	Ile	Ile
		115					120					125			
Phe	Ile	Thr	Ser	Ala	Ala	Pro	Phe	Gly	Pro	Trp	Lys	Glu	Leu	Ser	Thr
	130					135					140				
Tyr	Ser	Ser	Ala	Arg	Ala	Gly	Ala	Ser	Ala	Leu	Ala	Asn	Ala	Leu	Ser
145					150					155				160	
Lys	Glu	Leu	Gly	Glu	Tyr	Asn	Ile	Pro	Val	Phe	Ala	Ile	Gly	Pro	Asn
				165					170					175	
Tyr	Leu	His	Ser	Glu	Asp	Ser	Pro	Tyr	Tyr	Tyr	Pro	Thr	Glu	Pro	Trp
			180					185					190		
Lys	Ile	Asn	Pro	Glu	His	Val	Ala	His	Val	Lys	Lys	Val	Thr	Ala	Leu
		195					200					205			
Gln	Arg	Leu	Gly	Thr	Gln	Lys	Glu	Leu	Gly	Glu	Leu	Val	Ala	Phe	Leu
	210					215					220				
Ala	Ser	Gly	Ser	Cys	Asp	Tyr	Leu	Thr	Gly	Gln	Val	Phe	Trp	Leu	Ala
225					230					235				240	
Gly	Gly	Phe	Pro	Val	Ile	Glu	Arg	Trp	Pro	Gly	Met	Pro	Glu		
				245					250						

<210> 103  
 <211> 768  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HHDH S01009684

<221> CDS  
 <222> (1)...(765).

<400> 103	
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1 5 10 15	
agt gcg ctg aaa ctg tcg gag gcc ggt cat aca gta gcg tgt cac gat	96
Ser Ala Leu Lys Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	
gaa agt ttc aaa caa aag gac gaa ttg gaa gcc ttt gcg gaa act tac	144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	

35					40					45							
cca	cag	ctg	aaa	ccg	atg	tca	gaa	cag	gag	cca	gcg	gag	tta	att	gag	192	
Pro	Gln	Leu	Lys	Pro	Met	Ser	Glu	Gln	Glu	Pro	Ala	Glu	Leu	Ile	Glu		
50					55					60							
gcg	gtc	acc	agt	gcc	ttc	ggc	cag	gtg	gat	gtc	ctg	gtt	agc	aac	gac	240	
Ala	Val	Thr	Ser	Ala	Phe	Gly	Gln	Val	Asp	Val	Leu	Val	Ser	Asn	Asp		
65					70					75					80		
atc	ttt	gct	ctg	gaa	ttc	cag	ccg	att	gac	aag	tat	gcc	gtc	gaa	gac	288	
Ile	Phe	Ala	Leu	Glu	Phe	Gln	Pro	Ile	Asp	Lys	Tyr	Ala	Val	Glu	Asp		
85					90					95							
tac	cgt	ggc	gcg	gta	gaa	gca	ctg	cag	atc	aag	ccg	ttc	gcg	ttg	gtt	336	
Tyr	Arg	Gly	Ala	Val	Glu	Ala	Leu	Gln	Ile	Lys	Pro	Phe	Ala	Leu	Val		
100					105					110							
aat	gcc	gta	gct	agt	caa	atg	aaa	aaa	cgt	aaa	tca	ggc	cat	att	atc	384	
Asn	Ala	Val	Ala	Ser	Gln	Met	Lys	Lys	Arg	Lys	Ser	Gly	His	Ile	Ile		
115					120					125							
ttc	att	act	agc	gcg	gct	ccg	ttt	ggc	cca	tgg	aag	gag	ctg	tcg	act	432	
Phe	Ile	Thr	Ser	Ala	Ala	Pro	Phe	Gly	Pro	Trp	Lys	Glu	Leu	Ser	Thr		
130					135					140							
tat	agt	agt	gcg	cgc	gcc	ggg	gcc	tcc	gcg	ttg	gct	aac	gca	ctg	agt	480	
Tyr	Ser	Ser	Ala	Arg	Ala	Gly	Ala	Ser	Ala	Leu	Ala	Asn	Ala	Leu	Ser		
145					150					155					160		
aaa	gaa	tta	ggc	gag	tat	aat	atc	cct	gtt	ttc	gcc	att	ggg	cca	aac	528	
Lys	Glu	Leu	Gly	Glu	Tyr	Asn	Ile	Pro	Val	Phe	Ala	Ile	Gly	Pro	Asn		
165					170					175							
tat	ctg	cac	tca	gaa	gat	agc	cca	tac	tat	tac	cca	acg	gaa	ccg	tgg	576	
Tyr	Leu	His	Ser	Glu	Asp	Ser	Pro	Tyr	Tyr	Tyr	Pro	Thr	Glu	Pro	Trp		
180					185					190							
aag	atc	aac	cct	gaa	cat	gtg	gcg	cat	gtt	aaa	aaa	gta	aca	gcc	tta	624	
Lys	Ile	Asn	Pro	Glu	His	Val	Ala	His	Val	Lys	Lys	Val	Thr	Ala	Leu		
195					200					205							
caa	cgt	ctg	ggc	act	caa	aaa	gaa	ctt	ggc	gag	ctg	gtt	gcg	ttt	ctc	672	
Gln	Arg	Leu	Gly	Thr	Gln	Lys	Glu	Leu	Gly	Glu	Leu	Val	Ala	Phe	Leu		
210					215					220							
gct	tct	ggc	agc	tgc	gat	tac	ttg	acc	ggc	caa	gtc	ttc	tgg	tta	gcc	720	
Ala	Ser	Gly	Ser	Cys	Asp	Tyr	Leu	Thr	Gly	Gln	Val	Phe	Trp	Leu	Ala		
225					230					235					240		
ggc	ggc	ttt	ccg	gtg	att	gag	cgc	tgg	cca	ggc	atg	ccg	gaa	taa		765	
Gly	Gly	Phe	Pro	Val	Ile	Glu	Arg	Trp	Pro	Gly	Met	Pro	Glu	*			
245					250												
tga																768	
<210> 104																	

<211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HHDH S01009684

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 35 40 45  
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu  
 50 55 60  
 Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp  
 65 70 75 80  
 Ile Phe Ala Leu Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp  
 85 90 95  
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Lys Pro Phe Ala Leu Val  
 100 105 110  
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile  
 115 120 125  
 Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr  
 130 135 140  
 Tyr Ser Ser Ala Arg Ala Gly Ala Ser Ala Leu Ala Asn Ala Leu Ser  
 145 150 155 160  
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn  
 165 170 175  
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp  
 180 185 190  
 Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu  
 195 200 205  
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu  
 210 215 220  
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala  
 225 230 235 240  
 Gly Gly Phe Pro Val Ile Glu Arg Trp Pro Gly Met Pro Glu  
 245 250

<210> 105  
 <211> 774  
 <212> DNA  
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<220>  
 <223> HHDH S00817219

<221> CDS  
 <222> (1)...(765)

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 Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly  
 1 5 10 15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat	96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	
gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac	144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa	192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat	288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
ttc atc act tcg gct gct ccg ttc ggg cca tgg aag gag cta tcg act	432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
tac act tcg gct cga gct ggg gct tgt tcc cta gct aat gct cta tcg	480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Ser Leu Ala Asn Ala Leu Ser	
145 150 155 160	
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp	
180 185 190	
aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta	624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg	672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu	
210 215 220	
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca	720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala	
225 230 235 240	
ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa	765



Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu \*  
 245 250

tgaggatcc

774

<210> 106  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HHDH S00817219

<400> 106  
 Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly  
 1 5 10 15  
 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp  
 20 25 30  
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr  
 35 40 45  
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu  
 50 55 60  
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp  
 65 70 75 80  
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp  
 85 90 95  
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val  
 100 105 110  
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile  
 115 120 125  
 Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr  
 130 135 140  
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Ser Leu Ala Asn Ala Leu Ser  
 145 150 155 160  
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn  
 165 170 175  
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp  
 180 185 190  
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu  
 195 200 205  
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu  
 210 215 220  
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala  
 225 230 235 240  
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  
 245 250

<210> 107  
 <211> 774  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HHDH S00708827

<221> CDS  
 <222> (1)...(765)

<400> 107

atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt	48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly	
1 5 10 15	
agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat	96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	
gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac	144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gac ctg att gaa	192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Asp Leu Ile Glu	
50 55 60	
gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat	288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
aat gct gtg gct tcg caa atg aag aaa cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
ttc atc act tcg gct act ccg ttc ggg cca tgg aaa gag cta tcg act	432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg	480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser	
145 150 155 160	
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp	
180 185 190	
aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta	624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttc ctg	672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu	
210 215 220	

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca 720  
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala  
 225 230 235 240

ggc ggc ttt ccc ata ata gaa cgt tgg ccc ggc atg ccc gaa taa 765  
 Gly Gly Phe Pro Ile Ile Glu Arg Trp Pro Gly Met Pro Glu \*  
 245 250

tgaggatcc 774

<210> 108  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HHDH S00708827

<400> 108  
 Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly  
 1 5 10 15  
 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp  
 20 25 30  
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr  
 35 40 45  
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Asp Leu Ile Glu  
 50 55 60  
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp  
 65 70 75 80  
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp  
 85 90 95  
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val  
 100 105 110  
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile  
 115 120 125  
 Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr  
 130 135 140  
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser  
 145 150 155 160  
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn  
 165 170 175  
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp  
 180 185 190  
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu  
 195 200 205  
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu  
 210 215 220  
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala  
 225 230 235 240  
 Gly Gly Phe Pro Ile Ile Glu Arg Trp Pro Gly Met Pro Glu  
 245 250

<210> 109  
 <211> 765  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> HHDH S00772501

<221> CDS

<222> (1)...(765)

<400> 109

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Met	Ser	Thr	Ala	Ile	Val	Thr	Asn	Val	Lys	His	Phe	Gly	Gly	Met	Gly	
1				5					10					15		

agc	gct	ctg	agg	ctg	agc	gaa	gct	ggt	cat	acc	gtc	gct	tgc	cat	gat	96
Ser	Ala	Leu	Arg	Leu	Ser	Glu	Ala	Gly	His	Thr	Val	Ala	Cys	His	Asp	
		20						25					30			

gaa	agc	ttt	aaa	cag	aaa	gat	gaa	ctg	gaa	gct	ttt	gct	gaa	acc	tac	144
Glu	Ser	Phe	Lys	Gln	Lys	Asp	Glu	Leu	Glu	Ala	Phe	Ala	Glu	Thr	Tyr	
		35					40					45				

cca	cag	ctg	aaa	cca	atg	agc	gaa	cag	gaa	cca	gct	gaa	ctg	atc	gaa	192
Pro	Gln	Leu	Lys	Pro	Met	Ser	Glu	Gln	Glu	Pro	Ala	Glu	Leu	Ile	Glu	
	50					55					60					

gct	gtc	acc	agc	gct	ttt	ggt	cag	gtc	gat	gtc	ctg	gtc	agc	aac	gat	240
Ala	Val	Thr	Ser	Ala	Phe	Gly	Gln	Val	Asp	Val	Leu	Val	Ser	Asn	Asp	
65					70				75					80		

atc	ttt	gct	cca	gaa	ttt	cag	cca	atc	gat	aaa	tac	gct	gtc	gaa	gat	288
Ile	Phe	Ala	Pro	Glu	Phe	Gln	Pro	Ile	Asp	Lys	Tyr	Ala	Val	Glu	Asp	
			85					90						95		

tac	agg	ggt	gct	gtc	gaa	gct	ctg	cag	atc	agg	cca	ttt	gct	cta	gtg	336
Tyr	Arg	Gly	Ala	Val	Glu	Ala	Leu	Gln	Ile	Arg	Pro	Phe	Ala	Leu	Val	
			100					105					110			

aat	gct	gtg	gct	tcg	caa	atg	aag	aag	cga	aag	tcg	ggg	cac	atc	atc	384
Asn	Ala	Val	Ala	Ser	Gln	Met	Lys	Lys	Arg	Lys	Ser	Gly	His	Ile	Ile	
		115					120					125				

ttc	atc	act	tcg	gct	gcc	ccg	ttc	ggg	cca	tgg	aag	gag	cta	tcg	act	432
Phe	Ile	Thr	Ser	Ala	Ala	Pro	Phe	Gly	Pro	Trp	Lys	Glu	Leu	Ser	Thr	
	130					135					140					

tac	act	tcg	gct	cga	gct	ggg	gct	agt	act	cta	gct	aat	gct	cta	tcg	480
Tyr	Thr	Ser	Ala	Arg	Ala	Gly	Ala	Ser	Thr	Leu	Ala	Asn	Ala	Leu	Ser	
145					150					155				160		

aag	gag	cta	gga	gag	tac	aat	atc	ccg	gtg	ttc	gct	atc	ggg	ccg	aat	528
Lys	Glu	Leu	Gly	Glu	Tyr	Asn	Ile	Pro	Val	Phe	Ala	Ile	Gly	Pro	Asn	
			165						170					175		

tac	cta	cac	tcg	gag	gat	tcg	ccg	tac	ttc	tac	ccg	act	gag	ccg	tgg	576
Tyr	Leu	His	Ser	Glu	Asp	Ser	Pro	Tyr	Phe	Tyr	Pro	Thr	Glu	Pro	Trp	
			180					185					190			

aag	act	aat	ccg	gag	cac	gtg	gct	cac	gtg	aag	aag	gtg	act	gct	cta	624
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Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu  
 195 200 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg 672  
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu  
 210 215 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca 720  
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala  
 225 230 235 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa 765  
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu \*  
 245 250

<210> 110  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HHDH S00772501

<400> 110  
 Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly  
 1 5 10 15  
 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp  
 20 25 30  
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr  
 35 40 45  
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu  
 50 55 60  
 Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp  
 65 70 75 80  
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp  
 85 90 95  
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val  
 100 105 110  
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile  
 115 120 125  
 Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr  
 130 135 140  
 Tyr Thr Ser Ala Arg Ala Gly Ala Ser Thr Leu Ala Asn Ala Leu Ser  
 145 150 155 160  
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn  
 165 170 175  
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp  
 180 185 190  
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu  
 195 200 205  
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu  
 210 215 220  
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala  
 225 230 235 240  
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  
 245 250

<210> 111  
 <211> 762  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HHDH S01035968

<221> CDS  
 <222> (1)...(765)

<400> 111  
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 Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly  
 1 5 10 15  
 agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat 96  
 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp  
 20 25 30  
 gaa agc ttt aag cat aaa gat gaa ctg gaa gct ttt gct gaa acc tac 144  
 Glu Ser Phe Lys His Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr  
 35 40 45  
 cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa 192  
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu  
 50 55 60  
 gct gtc acc agc gct ttt ggt cag gtc gat gtc ctg gtc agc aac gat 240  
 Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp  
 65 70 75 80  
 atc ttt gct cta gaa ttt cgg cca atc gat aaa tac gct gtc gag gat 288  
 Ile Phe Ala Leu Glu Phe Arg Pro Ile Asp Lys Tyr Ala Val Glu Asp  
 85 90 95  
 tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg 336  
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val  
 100 105 110  
 aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc 384  
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile  
 115 120 125  
 ttc atc act tcg gct gcc ccg ttc ggg cca tgg aag gag cta tcg act 432  
 Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr  
 130 135 140  
 tac tct tcg gct cga gct ggg gct agt gca cta gct aat gct cta tcg 480  
 Tyr Ser Ser Ala Arg Ala Gly Ala Ser Ala Leu Ala Asn Ala Leu Ser  
 145 150 155 160  
 aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat 528  
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn  
 165 170 175

tac cta cac tcg gag gat tcg ccg tac tat tac ccc act gag ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp	
180 185 190	

aag att aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta	624
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg	672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu	
210 215 220	

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca	720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala	
225 230 235 240	

ggc ggc ttt ccc gtc ata gaa cgt tgg ccc ggc atg ccc gaa	762
Gly Gly Phe Pro Val Ile Glu Arg Trp Pro Gly Met Pro Glu	
245 250	

<210> 112  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HHDH S01035968

<400> 112	
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly	
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20 25 30	
Glu Ser Phe Lys His Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
Ile Phe Ala Leu Glu Phe Arg Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
Tyr Ser Ser Ala Arg Ala Gly Ala Ser Ala Leu Ala Asn Ala Leu Ser	
145 150 155 160	
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp	
180 185 190	
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu	

210	215	220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala		
225	230	235
Gly Gly Phe Pro Val Ile Glu Arg Trp Pro Gly Met Pro Glu		240
245	250	

<210> 113  
 <211> 852  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> KRED S01040430

<221> CDS  
 <222> (1)...(852)

<400> 113	
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Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Ala Pro Ala	
1 5 10 15	
cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac	96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn	
20 25 30	
ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg	144
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala	
35 40 45	
ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat	192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr	
50 55 60	
aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat	240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr	
65 70 75 80	
ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg	288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala	
85 90 95	
gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac	336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp	
100 105 110	
ata gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc	384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile	
115 120 125	
gat cag gat gac gat aaa cat ttt gac cag gtg gtt gac gtc gac ctg	432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu	
130 135 140	
aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa	480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu	
145 150 155 160	



cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtc ttt acg gct tcc	528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser	
165 170 175	
atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg gcc tac aat	576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Ala Tyr Asn	
180 185 190	
gcg gtc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa	624
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu	
195 200 205	
ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat	672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn	
210 215 220	
acc gag atc tct gat ttc gtc ccg caa gaa aca cag aat aaa tgg tgg	720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp	
225 230 235 240	
agc tta gtt cca ttg ggc cgt ggc ggg gaa act gcg gaa tta gtt ggt	768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly	
245 250 255	
gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc acg	816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr	
260 265 270	
gat atc att gtg gac ggc ggc tac acg ctg ccg tag	852
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro *	
275 280	

<210> 114  
 <211> 283  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> KRED S01040430

<400> 114

Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Ala Pro Ala	
1 5 10 15	
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn	
20 25 30	
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala	
35 40 45	
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr	
50 55 60	
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr	
65 70 75 80	
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala	
85 90 95	
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp	
100 105 110	

Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile  
 115 120 125  
 Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu  
 130 135 140  
 Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu  
 145 150 155 160  
 Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser  
 165 170 175  
 Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Ala Tyr Asn  
 180 185 190  
 Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu  
 195 200 205  
 Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn  
 210 215 220  
 Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp  
 225 230 235 240  
 Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly  
 245 250 255  
 Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr  
 260 265 270  
 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  
 275 280

<210> 115  
 <211> 852  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> KRED S01091361

<221> CDS  
 <222> (1)...(852)

<400> 115  
 atg gct aaa aac ttt tcc aat gtc gaa tat cct gcc ccg gcg cca gct 48  
 Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Ala Pro Ala  
 1 5 10 15  
  
 cat acc aaa gac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac 96  
 His Thr Lys Asp Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn  
 20 25 30  
  
 ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg 144  
 Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala  
 35 40 45  
  
 ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat 192  
 Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr  
 50 55 60  
  
 aac agt cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat 240  
 Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr  
 65 70 75 80  
  
 ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg 288  
 Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala

85										90					95					
gtg	aaa	cag	act	att	gag	cag	cag	atc	aag	gat	ttt	ggc	cac	ctg	gac	336				
Val	Lys	Gln	Thr	Ile	Glu	Gln	Gln	Ile	Lys	Asp	Phe	Gly	His	Leu	Asp					
		100						105					110							
ata	gtt	gtg	gcg	aac	gca	ggc	atc	cca	tgg	act	aag	ggg	gca	tac	atc	384				
Ile	Val	Val	Ala	Asn	Ala	Gly	Ile	Pro	Trp	Thr	Lys	Gly	Ala	Tyr	Ile					
		115					120						125							
gat	cag	gat	gac	gat	aaa	cat	ttt	gac	cag	gtg	gtg	gac	gtc	gac	ctg	432				
Asp	Gln	Asp	Asp	Asp	Lys	His	Phe	Asp	Gln	Val	Val	Asp	Val	Asp	Leu					
	130					135						140								
aaa	ggc	gca	ggc	tat	gta	gca	aaa	cat	gcg	ggg	cgc	cat	ttt	cgt	gaa	480				
Lys	Gly	Ala	Gly	Tyr	Val	Ala	Lys	His	Ala	Gly	Arg	His	Phe	Arg	Glu					
	145				150					155					160					
cgt	ttc	gaa	aaa	gaa	ggc	aaa	aag	ggc	gcc	ttg	gtc	ttt	acg	gct	tcc	528				
Arg	Phe	Glu	Lys	Glu	Gly	Lys	Lys	Gly	Ala	Leu	Val	Phe	Thr	Ala	Ser					
			165						170					175						
atg	tgc	ggg	cac	att	gtt	aat	gtg	ccg	caa	ttt	cag	gcg	acc	tac	aat	576				
Met	Ser	Gly	His	Ile	Val	Asn	Val	Pro	Gln	Phe	Gln	Ala	Thr	Tyr	Asn					
			180					185					190							
gcg	gtc	aag	gca	ggc	gtg	cgt	cat	ttc	gca	aag	tcc	ctg	gcc	gtg	gaa	624				
Ala	Val	Lys	Ala	Gly	Val	Arg	His	Phe	Ala	Lys	Ser	Leu	Ala	Val	Glu					
		195					200					205								
ttt	gct	cct	ttc	gca	cgt	gtt	aac	tct	gta	tct	cct	ggc	tat	att	aat	672				
Phe	Ala	Pro	Phe	Ala	Arg	Val	Asn	Ser	Val	Ser	Pro	Gly	Tyr	Ile	Asn					
	210					215					220									
acc	gag	atc	tct	gat	ttc	gtc	ccg	cag	gaa	aca	caa	aat	aaa	tgg	tgg	720				
Thr	Glu	Ile	Ser	Asp	Phe	Val	Pro	Gln	Glu	Thr	Gln	Asn	Lys	Trp	Trp					
	225				230				235					240						
agc	tta	gtt	cca	ttg	ggc	cgt	ggc	ggg	gaa	act	gcg	gaa	tta	gtt	ggg	768				
Ser	Leu	Val	Pro	Leu	Gly	Arg	Gly	Gly	Glu	Thr	Ala	Glu	Leu	Val	Gly					
			245					250					255							
gcc	tac	ctg	ttc	ctg	gca	agt	gat	gcg	ggc	tcc	tac	gcc	acg	ggc	acg	816				
Ala	Tyr	Leu	Phe	Leu	Ala	Ser	Asp	Ala	Gly	Ser	Tyr	Ala	Thr	Gly	Thr					
		260					265						270							
gat	atc	gtt	gtg	gac	ggc	ggc	tac	acg	ctg	ccg	tag					852				
Asp	Ile	Val	Val	Asp	Gly	Gly	Tyr	Thr	Leu	Pro	*									
		275					280													

<210> 116

<211> 283

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED S01091361

<400> 116

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 1          5          10          15
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 20          25          30
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
 35          40          45
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
 50          55          60
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
 65          70          75          80
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
 85          90          95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
 100         105         110
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
 115         120         125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
 130         135         140
Lys Gly Ala Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
 145         150         155         160
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
 165         170         175
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
 180         185         190
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
 195         200         205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
 210         215         220
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
 225         230         235         240
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
 245         250         255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
 260         265         270
Asp Ile Val Val Asp Gly Gly Tyr Thr Leu Pro
 275         280
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<210> 117

<211> 852

<212> DNA

<213> Artificial Sequence

<220>

<223> KRED S01091625

<221> CDS

<222> (1)...(852)

<400> 117

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Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Ala Pro Ala
 1          5          10          15
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48

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cat acc aag aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac
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96

His	Thr	Lys	Asn	Glu	Ser	Leu	Gln	Val	Leu	Asp	Leu	Phe	Lys	Leu	Asn	
			20					25					30			
ggc	aaa	gtc	gcg	tct	atc	acc	ggt	agc	aac	tca	ggc	att	ggt	tac	gcg	144
Gly	Lys	Val	Ala	Ser	Ile	Thr	Gly	Ser	Asn	Ser	Gly	Ile	Gly	Tyr	Ala	
		35					40					45				
ctg	gcc	gaa	gct	ttt	gcg	cag	gtt	ggc	gca	gac	gtt	gcg	atc	tgg	tat	192
Leu	Ala	Glu	Ala	Phe	Ala	Gln	Val	Gly	Ala	Asp	Val	Ala	Ile	Trp	Tyr	
		50					55					60				
aac	agt	cat	gat	gcc	acc	ggt	aaa	gca	gag	gcc	ctg	gct	aaa	aaa	tat	240
Asn	Ser	His	Asp	Ala	Thr	Gly	Lys	Ala	Glu	Ala	Leu	Ala	Lys	Lys	Tyr	
	65					70				75					80	
ggc	gta	aaa	gtc	aag	gct	tat	aaa	gct	aat	gtc	agc	tcg	agt	gat	gcg	288
Gly	Val	Lys	Val	Lys	Ala	Tyr	Lys	Ala	Asn	Val	Ser	Ser	Ser	Asp	Ala	
				85					90					95		
gtg	aaa	cag	act	att	gag	cag	cag	atc	aag	gat	ttt	ggc	cac	ctg	gac	336
Val	Lys	Gln	Thr	Ile	Glu	Gln	Gln	Ile	Lys	Asp	Phe	Gly	His	Leu	Asp	
			100					105					110			
ata	gtt	gtg	gcg	aac	gca	ggc	atc	cca	tgg	act	aag	ggt	gca	tac	atc	384
Ile	Val	Val	Ala	Asn	Ala	Gly	Ile	Pro	Trp	Thr	Lys	Gly	Ala	Tyr	Ile	
			115				120						125			
gat	cag	gat	gac	gat	aaa	cat	ttt	gac	cag	gtg	gtg	gac	gtc	gac	ctg	432
Asp	Gln	Asp	Asp	Asp	Lys	His	Phe	Asp	Gln	Val	Val	Asp	Val	Asp	Leu	
		130				135						140				
aaa	ggc	gca	ggc	tat	gta	gca	aaa	cat	gcg	ggt	cgc	cat	ttt	cgt	gaa	480
Lys	Gly	Ala	Gly	Tyr	Val	Ala	Lys	His	Ala	Gly	Arg	His	Phe	Arg	Glu	
	145					150				155					160	
cgt	ttc	gag	aaa	gaa	ggc	aaa	aag	ggc	gcc	ttg	gtc	ttt	acg	gct	tcc	528
Arg	Phe	Glu	Lys	Glu	Gly	Lys	Lys	Gly	Ala	Leu	Val	Phe	Thr	Ala	Ser	
				165				170						175		
atg	tcg	ggt	cac	atc	gtt	aat	gtg	ccg	caa	ttt	cag	gcg	acc	tac	aat	576
Met	Ser	Gly	His	Ile	Val	Asn	Val	Pro	Gln	Phe	Gln	Ala	Thr	Tyr	Asn	
			180					185					190			
gcg	gtc	aag	gca	ggc	gtg	cgt	cat	ttc	gca	aag	tcc	ctg	gcc	gtg	gaa	624
Ala	Val	Lys	Ala	Gly	Val	Arg	His	Phe	Ala	Lys	Ser	Leu	Ala	Val	Glu	
			195				200						205			
ttt	gct	cct	ttc	gca	cgt	gtt	aac	tct	gta	tct	cct	ggc	tat	att	aat	672
Phe	Ala	Pro	Phe	Ala	Arg	Val	Asn	Ser	Val	Ser	Pro	Gly	Tyr	Ile	Asn	
		210					215					220				
acc	gag	atc	tct	gat	ttc	gtc	ccg	caa	gaa	aca	caa	aat	aga	tgg	tgg	720
Thr	Glu	Ile	Ser	Asp	Phe	Val	Pro	Gln	Glu	Thr	Gln	Asn	Arg	Trp	Trp	
	225					230				235					240	
agc	tta	gtt	cca	ttg	ggc	cgt	ggc	ggg	gaa	act	gcg	gaa	tta	gtt	ggt	768
Ser	Leu	Val	Pro	Leu	Gly	Arg	Gly	Gly	Glu	Thr	Ala	Glu	Leu	Val	Gly	

245	250	255	
gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca			816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr			
260	265	270	

gat atc att gtg gac ggc ggc tac acg ctg ccg tag	852
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro *	
275 280	

<210> 118  
 <211> 283  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> KRED S01091625

<400> 118

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His	Thr	Lys	Asn	Glu	Ser	Leu	Gln	Val	Leu	Asp	Leu	Phe	Lys	Leu	Asn
			20					25					30		
Gly	Lys	Val	Ala	Ser	Ile	Thr	Gly	Ser	Asn	Ser	Gly	Ile	Gly	Tyr	Ala
		35					40					45			
Leu	Ala	Glu	Ala	Phe	Ala	Gln	Val	Gly	Ala	Asp	Val	Ala	Ile	Trp	Tyr
	50					55				60					
Asn	Ser	His	Asp	Ala	Thr	Gly	Lys	Ala	Glu	Ala	Leu	Ala	Lys	Lys	Tyr
65				70					75					80	
Gly	Val	Lys	Val	Lys	Ala	Tyr	Lys	Ala	Asn	Val	Ser	Ser	Ser	Asp	Ala
			85						90					95	
Val	Lys	Gln	Thr	Ile	Glu	Gln	Gln	Ile	Lys	Asp	Phe	Gly	His	Leu	Asp
		100						105					110		
Ile	Val	Val	Ala	Asn	Ala	Gly	Ile	Pro	Trp	Thr	Lys	Gly	Ala	Tyr	Ile
		115					120					125			
Asp	Gln	Asp	Asp	Asp	Lys	His	Phe	Asp	Gln	Val	Val	Asp	Val	Asp	Leu
	130				135					140					
Lys	Gly	Ala	Gly	Tyr	Val	Ala	Lys	His	Ala	Gly	Arg	His	Phe	Arg	Glu
145				150					155					160	
Arg	Phe	Glu	Lys	Glu	Gly	Lys	Lys	Gly	Ala	Leu	Val	Phe	Thr	Ala	Ser
			165					170						175	
Met	Ser	Gly	His	Ile	Val	Asn	Val	Pro	Gln	Phe	Gln	Ala	Thr	Tyr	Asn
		180					185					190			
Ala	Val	Lys	Ala	Gly	Val	Arg	His	Phe	Ala	Lys	Ser	Leu	Ala	Val	Glu
	195				200							205			
Phe	Ala	Pro	Phe	Ala	Arg	Val	Asn	Ser	Val	Ser	Pro	Gly	Tyr	Ile	Asn
	210				215						220				
Thr	Glu	Ile	Ser	Asp	Phe	Val	Pro	Gln	Glu	Thr	Gln	Asn	Arg	Trp	Trp
225				230					235					240	
Ser	Leu	Val	Pro	Leu	Gly	Arg	Gly	Gly	Glu	Thr	Ala	Glu	Leu	Val	Gly
			245					250					255		
Ala	Tyr	Leu	Phe	Leu	Ala	Ser	Asp	Ala	Gly	Ser	Tyr	Ala	Thr	Gly	Thr
		260					265						270		
Asp	Ile	Ile	Val	Asp	Gly	Gly	Tyr	Thr	Leu	Pro					
	275						280								

<210> 119  
 <211> 852  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> KRED S01094648

<221> CDS  
 <222> (1)...(852)

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 cat acc aaa agc gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac 96  
 His Thr Lys Ser Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn  
 20 25 30  
 ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg 144  
 Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala  
 35 40 45  
 ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat 192  
 Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr  
 50 55 60  
 aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat 240  
 Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr  
 65 70 75 80  
 ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg 288  
 Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala  
 85 90 95  
 gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac 336  
 Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp  
 100 105 110  
 ata gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc 384  
 Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile  
 115 120 125  
 gat cag gat gac gat aaa cat ttt gac cag gtg gtt gac gtc gac ctg 432  
 Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu  
 130 135 140  
 aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa 480  
 Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu  
 145 150 155 160  
 cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtc ttt acg gct tcc 528  
 Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser  
 165 170 175  
 atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg gcc tac aat 576

Met	Ser	Gly	His	Ile	Val	Asn	Val	Pro	Gln	Phe	Gln	Ala	Ala	Tyr	Asn	
			180					185					190			
gcg	gtc	aag	gca	ggc	gtg	cgt	cat	ttc	gca	aag	tcc	ctg	gcc	gtg	gaa	624
Ala	Val	Lys	Ala	Gly	Val	Arg	His	Phe	Ala	Lys	Ser	Leu	Ala	Val	Glu	
		195					200					205				
ttt	gct	cct	ttc	gca	cgt	gtt	aac	tct	gta	tct	cct	ggc	tat	att	aat	672
Phe	Ala	Pro	Phe	Ala	Arg	Val	Asn	Ser	Val	Ser	Pro	Gly	Tyr	Ile	Asn	
	210					215					220					
acc	gag	atc	tct	gat	ttc	gtc	ccg	caa	gga	aca	cag	aat	aaa	tgg	tgg	720
Thr	Glu	Ile	Ser	Asp	Phe	Val	Pro	Gln	Gly	Thr	Gln	Asn	Lys	Trp	Trp	
225					230				235					240		
agc	tta	gtt	cca	ttg	ggc	cgt	ggc	ggg	gaa	act	gcg	gaa	tta	gtt	ggc	768
Ser	Leu	Val	Pro	Leu	Gly	Arg	Gly	Gly	Glu	Thr	Ala	Glu	Leu	Val	Gly	
			245						250					255		
gcc	tac	ctg	ttc	ctg	gca	agt	gat	gcg	ggc	tcc	tac	gcc	acg	ggc	acg	816
Ala	Tyr	Leu	Phe	Leu	Ala	Ser	Asp	Ala	Gly	Ser	Tyr	Ala	Thr	Gly	Thr	
		260						265					270			
gat	atc	att	gtg	gac	ggc	ggc	tac	acg	ctg	ccg	tag					852
Asp	Ile	Ile	Val	Asp	Gly	Gly	Tyr	Thr	Leu	Pro	*					
		275					280									

<210> 120  
 <211> 283  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> KRED S01094648

Met	Ala	Lys	Asn	Phe	Ser	Asn	Val	Gly	Tyr	Pro	Ala	Pro	Ala	Pro	Ala	
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His	Thr	Lys	Ser	Glu	Ser	Leu	Gln	Val	Leu	Asp	Leu	Phe	Lys	Leu	Asn	
		20					25					30				
Gly	Lys	Val	Ala	Ser	Ile	Thr	Gly	Ser	Asn	Ser	Gly	Ile	Gly	Tyr	Ala	
	35					40					45					
Leu	Ala	Glu	Ala	Phe	Ala	Gln	Val	Gly	Ala	Asp	Val	Ala	Ile	Trp	Tyr	
	50				55				60							
Asn	Ser	His	Asp	Ala	Thr	Gly	Lys	Ala	Glu	Ala	Leu	Ala	Lys	Lys	Tyr	
65				70					75					80		
Gly	Val	Lys	Val	Lys	Ala	Tyr	Lys	Ala	Asn	Val	Ser	Ser	Ser	Asp	Ala	
			85					90					95			
Val	Lys	Gln	Thr	Ile	Glu	Gln	Gln	Ile	Lys	Asp	Phe	Gly	His	Leu	Asp	
		100					105					110				
Ile	Val	Val	Ala	Asn	Ala	Gly	Ile	Pro	Trp	Thr	Lys	Gly	Ala	Tyr	Ile	
	115					120						125				
Asp	Gln	Asp	Asp	Asp	Lys	His	Phe	Asp	Gln	Val	Val	Asp	Val	Asp	Leu	
	130				135				140							
Lys	Gly	Val	Gly	Tyr	Val	Ala	Lys	His	Ala	Gly	Arg	His	Phe	Arg	Glu	
145					150				155						160	



Arg	Phe	Glu	Lys	Glu	Gly	Lys	Lys	Gly	Ala	Leu	Val	Phe	Thr	Ala	Ser	
				165					170						175	
Met	Ser	Gly	His	Ile	Val	Asn	Val	Pro	Gln	Phe	Gln	Ala	Ala	Tyr	Asn	
			180					185					190			
Ala	Val	Lys	Ala	Gly	Val	Arg	His	Phe	Ala	Lys	Ser	Leu	Ala	Val	Glu	
		195					200					205				
Phe	Ala	Pro	Phe	Ala	Arg	Val	Asn	Ser	Val	Ser	Pro	Gly	Tyr	Ile	Asn	
	210				215						220					
Thr	Glu	Ile	Ser	Asp	Phe	Val	Pro	Gln	Gly	Thr	Gln	Asn	Lys	Trp	Trp	
225				230						235					240	
Ser	Leu	Val	Pro	Leu	Gly	Arg	Gly	Gly	Glu	Thr	Ala	Glu	Leu	Val	Gly	
			245					250						255		
Ala	Tyr	Leu	Phe	Leu	Ala	Ser	Asp	Ala	Gly	Ser	Tyr	Ala	Thr	Gly	Thr	
		260					265						270			
Asp	Ile	Ile	Val	Asp	Gly	Gly	Tyr	Thr	Leu	Pro						
	275						280									

<210> 121  
 <211> 789  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> GDH S01024744

<221> CDS  
 <222> (1)...(789)

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Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala	
1 5 10 15	
tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag gag cag gca	96
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala	
20 25 30	
aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg aac gag gta	144
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val	
35 40 45	
aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc gtc caa gga	192
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly	
50 55 60	
gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa acg gca att	240
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile	
65 70 75 80	
aag gag ttc ggc aca ctc gat att atg att aat aat gcc ggt ctt gaa	288
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu	
85 90 95	
aat cct gtg cca tct cac gaa atg ccg ctc aag gat tgg gat aaa gtc	336
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val	
100 105 110	

atc ggc acg aac tta acg ggt gcc ttt tta gga agc cgt gaa gcg att	384
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile	
115 120 125	
aaa tat ttc gta gaa aac gat atc aag gga aat gtc att aac atg tcc	432
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser	
130 135 140	
agt gtg cac gaa gtg att cct tgg cca tta ttt gtc cac tat gcg gca	480
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala	
145 150 155 160	
agt aaa ggc ggg atg aag ctg atg aca gaa aca tta gcg ttg gaa tac	528
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr	
165 170 175	
gcg ccg aag ggc att cgc gtc aat aat att ggg cca ggt gcg atc aac	576
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn	
180 185 190	
acg acg atc aat aag gag aaa ttt gct gac cct gaa cag aga gct gat	624
Thr Thr Ile Asn Lys Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp	
195 200 205	
gta gaa agc atg att cca atg gga tat atc ggc gaa ccg gag gag atc	672
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile	
210 215 220	
gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc agc tac gtc aca	720
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr	
225 230 235 240	
ggc atc acg tta ttc gcg gac ggc ggt atg aca caa tat cct tca ttc	768
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe	
245 250 255	
cag gca ggc cgc ggt taa tga	789
Gln Ala Gly Arg Gly * *	
260	

<210> 122

<211> 261

<212> PRT

<213> Artificial Sequence

<220>

<223> GDH S01024744

<400> 122

Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala	
1 5 10 15	
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala	
20 25 30	
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val	
35 40 45	
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly	

50		55		60
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile				
65		70		75
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu				80
	85		90	95
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val				
	100		105	110
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile				
	115		120	125
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser				
	130		135	140
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala				
	145		150	155
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr				160
	165		170	175
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn				
	180		185	190
Thr Thr Ile Asn Lys Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp				
	195		200	205
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile				
	210		215	220
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr				
	225		230	235
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe				240
	245		250	255
Gln Ala Gly Arg Gly				
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<210> 123

<211> 789

<212> DNA

<213> Artificial Sequence

<220>

<223> GDH S01052992

<221> CDS

<222> (1)...(789)

<400> 123

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tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag gag cag gca	96
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala	
20 25 30	
aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg aac gag gta	144
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val	
35 40 45	
aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc gtc caa gga	192
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly	
50 55 60	
gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa acg gca att	240



<220>

<223> GDH S01052992

<400> 124

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      20          25          30
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
      35          40          45
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
      50          55          60
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
      65          70          75          80
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
      85          90          95
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
      100          105          110
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
      115          120          125
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
      130          135          140
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
      145          150          155          160
Ser Lys Gly Gly Met Lys Leu Met Thr Lys Thr Leu Ala Leu Glu Tyr
      165          170          175
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
      180          185          190
Thr Thr Ile Asn Lys Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp
      195          200          205
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Asp Glu Ile
      210          215          220
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Cys Tyr Val Thr
      225          230          235          240
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
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<210> 125

<211> 789

<212> DNA

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<220>

<223> GDH S01063714

<221> CDS

<222> (1)...(789)

<400> 125

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Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Thr
 1          5          10          15

tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag gag cag gca
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
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48

96

20	25	30	
aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg aac gag gta Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val 35 40 45			144
aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc gtc caa gga Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly 50 55 60			192
gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa acg gca att Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile 65 70 75 80			240
aag gag ttc ggc aca ctc gat att atg att aat aat gcc ggt ctt gaa Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu 85 90 95			288
aat cct gtg cca tct cac gaa atg ccg ctc aag gat tgg gat aaa gtc Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val 100 105 110			336
atc ggc acg aac tta acg ggt gcc ttt tta gga agc cgt gaa gcg att Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile 115 120 125			384
aaa tat ttc gta gaa aac gat atc aag gga aat gtc att aac atg tcc Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser 130 135 140			432
agt gtg cac gaa gtg att cct tgg cca tta ttt gtc cac tat gcg gca Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala 145 150 155 160			480
agt aaa ggc ggg atg aag ctg atg aca gaa aca tta gcg ttg gaa tac Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr 165 170 175			528
gcg ccg aag ggc att cgc gtc aat aat att ggg cca ggt gcg atc aac Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn 180 185 190			576
acg acg atc aat aag gag aaa ttt gct gac cct gaa cag aga gct gat Thr Thr Ile Asn Lys Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp 195 200 205			624
gta gaa agc atg att cca atg gga tat atc ggc gaa ccg gag gag atc Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile 210 215 220			672
gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc agc tac gtc aca Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr 225 230 235 240			720
ggc atc acg tta ttc gcg gac ggc ggt atg aca caa tat cct tca ttc Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe 245 250 255			768

cag gca ggc cgc ggt taa tga  
 Gln Ala Gly Arg Gly \* \*  
 260

789

<210> 126  
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 <212> PRT  
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<400> 126

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			20					25					30		
Lys	Val	Val	Ile	Asn	Tyr	Tyr	Ser	Asn	Lys	Gln	Asp	Pro	Asn	Glu	Val
		35					40					45			
Lys	Glu	Glu	Val	Ile	Lys	Ala	Gly	Gly	Glu	Ala	Val	Val	Val	Gln	Gly
	50					55					60				
Asp	Val	Thr	Lys	Glu	Glu	Asp	Val	Lys	Asn	Ile	Val	Gln	Thr	Ala	Ile
65					70					75				80	
Lys	Glu	Phe	Gly	Thr	Leu	Asp	Ile	Met	Ile	Asn	Asn	Ala	Gly	Leu	Glu
				85					90					95	
Asn	Pro	Val	Pro	Ser	His	Glu	Met	Pro	Leu	Lys	Asp	Trp	Asp	Lys	Val
		100						105					110		
Ile	Gly	Thr	Asn	Leu	Thr	Gly	Ala	Phe	Leu	Gly	Ser	Arg	Glu	Ala	Ile
		115				120						125			
Lys	Tyr	Phe	Val	Glu	Asn	Asp	Ile	Lys	Gly	Asn	Val	Ile	Asn	Met	Ser
	130					135					140				
Ser	Val	His	Glu	Val	Ile	Pro	Trp	Pro	Leu	Phe	Val	His	Tyr	Ala	Ala
145					150					155					160
Ser	Lys	Gly	Gly	Met	Lys	Leu	Met	Thr	Glu	Thr	Leu	Ala	Leu	Glu	Tyr
				165					170					175	
Ala	Pro	Lys	Gly	Ile	Arg	Val	Asn	Asn	Ile	Gly	Pro	Gly	Ala	Ile	Asn
			180					185					190		
Thr	Thr	Ile	Asn	Lys	Glu	Lys	Phe	Ala	Asp	Pro	Glu	Gln	Arg	Ala	Asp
		195					200					205			
Val	Glu	Ser	Met	Ile	Pro	Met	Gly	Tyr	Ile	Gly	Glu	Pro	Glu	Glu	Ile
	210					215					220				
Ala	Ala	Val	Ala	Ala	Trp	Leu	Ala	Ser	Lys	Glu	Ala	Ser	Tyr	Val	Thr
225					230					235					240
Gly	Ile	Thr	Leu	Phe	Ala	Asp	Gly	Gly	Met	Thr	Gln	Tyr	Pro	Ser	Phe
				245					250					255	
Gln	Ala	Gly	Arg	Gly											
				260											